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OM protein - protein search, using sw model

Run on: August 10, 2004, 15:55:40 ; Search time 80.4324 Seconds
(without alignments)
217.797 Million cell updates/sec

Title: US-10-072-602B-352

Perfect score: 331

Sequence: 1 MRCLPVFVILLTASGPSV.....LQRHQDKSVCCGYKLCFPGC 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	331	100.0	62	5	ABG99600	Abg99600 Conus sp
2	298	90.0	62	5	ABG99591	Abg99591 Conus sp
3	286	86.4	62	5	ABG99589	Abg99589 Conus sp
4	281	84.9	62	5	ABG99517	Abg99517 Conus sp
5	281	84.9	62	5	ABG99604	Abg99604 Conus sp
6	272	82.2	64	5	ABG99593	Abg99593 Conus sp
7	266	80.4	62	5	ABG99606	Abg99606 Conus sp
8	264	79.8	64	5	ABG99470	Abg99470 Conus sp
9	264	79.8	64	5	ABG99587	Abg99587 Conus sp
10	264	79.8	64	5	ABG99608	Abg99608 Conus sp
11	254.5	76.9	61	5	ABG99561	Abg99561 Conus sp
12	253.5	76.6	61	5	ABG99612	Abg99612 Conus sp
13	220	66.5	60	5	ABG99569	Abg99569 Conus sp
14	216	65.3	61	5	ABG99400	Abg99400 Conus sp
15	216	65.3	61	5	ABG99598	Abg99598 Conus sp
16	211.5	63.9	61	5	ABG99551	Abg99551 Conus sp
17	208	62.8	61	5	ABG99571	Abg99571 Conus sp
18	206	62.2	59	3	AA97123	AA97123 Tau conot
19	201.5	60.9	62	5	ABG99557	Abg99557 Conus sp
20	200	60.4	58	5	ABG99559	Abg99559 Conus sp
21	199	60.1	60	3	AA97124	AA97124 Tau conot
22	199	60.1	70	3	AA97122	AA97122 Tau conot
23	192	58.0	61	5	ABG99585	Abg99585 Conus sp
24	191	57.7	61	3	AA08016	AA08016 Amino aci
25	191	57.7	61	5	ABG99595	Abg99595 Conus sp

ALIGNMENTS

RESULT 1

ABG99600

ID ABG99600 standard; protein; 62 AA.

XX AC ABG99600;

XX DT 17-JAN-2003 (first entry)

XX DE Conus sp conotoxin-associated protein SEQ ID 352.

XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;

XX KW ligand-gated ion channel modulator; pain-relief.

XX OS Conus aulicus.

XX PN WO200264740-A2.

XX PD 22-AUG-2002.

XX PF 11-FEB-2002; 2002WO-US003887.

XX PR 09-FEB-2001; 2001US-0267408P.

XX PA (COGN-) COGNETIX INC.
(UTAH) UNIV UTAH RES FOUND.

XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;

XX PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

XX DR WPI, 2002-706921/76.

XX DR N-PSDB; ABX04937.

XX PT New cone snail conotoxin peptides, useful as a pain reliever for
alleviating pain in an individual suffering from pain or who is about to
be subjected to a pain-causing event, or for treating voltage-gated ion
channel disorders.

XX PS Claim 1; Page 239; 305pp; English.

XX CC This invention describes novel conotoxin peptides from the cone snail,
genus Conus which have analgesic activity and can act as a voltage-gated
ion channel modulator or a ligand-gated ion channel modulator. The
conotoxin peptide is useful as a pain-relieving agent for alleviating
pain in an individual who is either exhibiting pain or is about to be
subjected to a pain-causing event. The conotoxin peptide is also useful
for treating or preventing disorders associated with voltage-gated ion
channel disorders, ligand-gated ion channel disorders or receptor
disorders. The radiolabeled conotoxin peptide is also useful for

AA992231 Chi-conot
Abg99555 Conus sp
AA97129 Tau conot
Abg99563 Conus sp
AA97126 Tau conot
Abg99567 Conus sp
Abg99565 Conus sp
AA97115 Tau conot
AA97117 Tau conot
AA97125 Tau conot
AA97120 Tau conot
AA97121 Tau conot
AA97127 Tau conot
Abg99549 Conus sp
AA97116 Tau conot
AA97119 Tau conot
AA97128 Tau conot
Abg99553 Conus sp
AA97118 Tau conot
Abg99749 Conus sp

26 189 57.1 61 3 AA92231
27 188 56.8 63 5 ABG99555
28 180.5 54.5 62 3 AA97129
29 180 54.4 59 5 ABG99563
30 179 54.1 63 3 AA97126
31 176 53.2 60 5 ABG99567
32 175 52.9 59 5 ABG99565
33 169.5 51.2 62 3 AA97115
34 169 51.1 62 3 AA97117
35 167.5 50.6 64 3 AA97125
36 167 50.5 67 3 AA97120
37 166 50.2 67 3 AA97121
38 164 49.5 62 3 AA97127
39 163.5 49.4 64 5 ABG99549
40 151.5 45.8 61 3 AA97116
41 151.5 45.8 61 3 AA97119
42 148 44.7 63 3 AA97128
43 130 39.3 61 5 ABG99553
44 129.5 39.1 62 3 AA97118
45 79 23.9 12 5 ABG99749

CC characterising a new site on these receptors or channels, and for
CC screening and identifying novel small molecules that interact with the
CC above-mentioned channels or receptors, which are monoamine transporters.
CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
CC in the disclosure of the invention
XX
SQ Sequence 62 AA;

Query Match 100.0%; Score 331; DB 5; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.8e-35;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCPLPVFVILLITASGSDVRLKTKDDVPLSSFRDNAKSTLQRHDKSVCCGYKLCFP 60
DB 1 MRCPLPVFVILLITASGSDVRLKTKDDVPLSSFRDNAKSTLQRHDKSVCCGYKLCFP 60

QY 61 CG 62
DB 61 CG 62

RESULT 2
ABG99591
ID ABG99591 standard; protein; 62 AA.
XX AC ABG99591;
XX DT 17-JAN-2003 (first entry)
XX DE Conus sp conotoxin-associated protein SEQ ID 339.
XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
XX KW ligand-gated ion channel modulator; pain-relief.
XX OS Conus pennaceus.
XX PN WO200264740-A2.
XX PD 22-AUG-2002.
XX PF 11-FEB-2002; 2002WO-US003887.
XX PR 09-FEB-2001; 2001US-0267408P.
XX PA (COGN-) COGNETIX INC.
XX PA (UTAH) UNIV UTAH RES FOUND.
XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
XX PI Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
XX N-PSDB; ABX04933.
XX WPI; 2002-706921/76.
XX New cone snail conotoxin peptides, useful as a pain reliever for
PT alleviating pain in an individual suffering from pain or who is about to
PT be subjected to a pain-causing event, or for treating voltage-gated ion
PT channel disorders.
XX
PS Claim 1; Page 234; 305pp; English.
XX
CC This invention describes novel conotoxin peptides from the cone snail,
CC genus Conus which have analgesic activity and can act as a voltage-gated
CC ion channel modulator or a ligand-gated ion channel modulator. The
CC conotoxin peptide is useful as a pain-relieving agent for alleviating
CC pain in an individual who is either exhibiting pain or is about to be
CC subjected to a pain-causing event. The conotoxin peptide is also useful
CC for treating or preventing disorders associated with voltage-gated ion
CC channel disorders, ligand-gated ion channel disorders or receptor
CC disorders. The radiolabeled conotoxin peptide is also useful for
CC characterising a new site on these receptors or channels, and for
CC screening and identifying novel small molecules that interact with the
CC above-mentioned channels or receptors, which are monoamine transporters.
CC ABG99360-ABG99853 represent the conotoxin protein and peptides described

CC in the disclosure of the invention
XX
SQ Sequence 62 AA;

Query Match 90.0%; Score 298; DB 5; Length 62;
Best Local Similarity 88.7%; Pred. No. 9.9e-31;
Matches 55; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCPLPVFVILLITASGSDVRLKTKDDVPLSSFRDNAKSTLQRHDKSVCCGYKLCFP 60
DB 1 MRCPLPVFVILLITASGSDVRLKTKDDVPLSSFRDNAKSTLQRHDKSVCCGYKLCFP 60

QY 61 CG 62
DB 61 CG 62

RESULT 3
ABG99589
ID ABG99589 standard; protein; 62 AA.
XX AC ABG99589;
XX DT 17-JAN-2003 (first entry)
XX DE Conus sp conotoxin-associated protein SEQ ID 336.
XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
XX KW ligand-gated ion channel modulator; pain-relief.
XX OS Conus pennaceus.
XX PN WO200264740-A2.
XX PD 22-AUG-2002.
XX PF 11-FEB-2002; 2002WO-US003887.
XX PR 09-FEB-2001; 2001US-0267408P.
XX PA (COGN-) COGNETIX INC.
XX PA (UTAH) UNIV UTAH RES FOUND.
XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
XX PI Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
XX N-PSDB; ABX04933.
XX WPI; 2002-706921/76.
XX New cone snail conotoxin peptides, useful as a pain reliever for
PT alleviating pain in an individual suffering from pain or who is about to
PT be subjected to a pain-causing event, or for treating voltage-gated ion
PT channel disorders.
XX
PS Claim 1; Page 233; 305pp; English.
XX
CC This invention describes novel conotoxin peptides from the cone snail,
CC genus Conus which have analgesic activity and can act as a voltage-gated
CC ion channel modulator or a ligand-gated ion channel modulator. The
CC conotoxin peptide is useful as a pain-relieving agent for alleviating
CC pain in an individual who is either exhibiting pain or is about to be
CC subjected to a pain-causing event. The conotoxin peptide is also useful
CC for treating or preventing disorders associated with voltage-gated ion
CC channel disorders, ligand-gated ion channel disorders or receptor
CC disorders. The radiolabeled conotoxin peptide is also useful for
CC characterising a new site on these receptors or channels, and for
CC screening and identifying novel small molecules that interact with the
CC above-mentioned channels or receptors, which are monoamine transporters.
CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
CC in the disclosure of the invention
XX
SQ Sequence 62 AA;

Query Match 86.4%; Score 286; DB 5; Length 62;
 Best Local Similarity 88.5%; Pred. No. 3.2e-29;
 Matches 54; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRCPLPVFVILLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60
 DB 1 MRCPLPVFVILLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60

QY 61 C 61
 DB 61 C 61

RESULT 4
 ABG99517
 ID ABG99517 standard; protein; 62 AA.

AC ABG99517;
 DT 17-JAN-2003 (first entry)
 DE Conus sp conotoxin-associated protein SEQ ID 229.
 XX Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 KW ligand-gated ion channel modulator; pain-relief.
 XX Conus textile.
 OS WO200264740-A2.
 PN 22-AUG-2002.
 XX 11-FEB-2002; 2002WO-US003887.
 XX 09-FEB-2001; 2001US-0267408P.
 XX (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX N-PSDB; ABX04897.

XX WPI; 2002-706921/76.
 DR New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX Claim 1; Page 195; 305pp; English.

XX This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterising a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX Sequence 62 AA;

Query Match 84.9%; Score 281; DB 5; Length 62;
 Best Local Similarity 82.3%; Pred. No. 1.4e-28;
 Matches 51; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRCPLPVFVILLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60
 DB 1 MRCPLPVFVILLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60

QY 61 CG 62
 DB 61 CG 62

RESULT 5
 ABG99604
 ID ABG99604 standard; protein; 62 AA.

XX ABG99604;
 DT 17-JAN-2003 (first entry)
 DE Conus sp conotoxin-associated protein SEQ ID 358.
 XX Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 KW ligand-gated ion channel modulator; pain-relief.
 XX Conus textile.
 OS WO200264740-A2.
 PN 22-AUG-2002.
 XX 11-FEB-2002; 2002WO-US003887.
 XX 09-FEB-2001; 2001US-0267408P.
 XX (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX N-PSDB; ABX04939.

XX WPI; 2002-706921/76.
 DR New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX Claim 1; Page 240; 305pp; English.

XX This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterising a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX Sequence 62 AA;

Query Match 84.9%; Score 281; DB 5; Length 62;
 Best Local Similarity 82.3%; Pred. No. 1.4e-28;
 Matches 51; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRCPLPVFVILLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60
 DB 1 MRCPLPVFVILLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60

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QY      61 CG 62
Db      61 CG 62

RESULT 6
ABG99593
ID  ABG99593 standard; protein; 64 AA.
XX  AC  ABG99593;
XX  DT  17-JAN-2003 (first entry)
XX  DE  Conus sp conotoxin-associated protein SEQ ID 342.
XX  KW  Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
XX  KW  ligand-gated ion channel modulator; pain-relief.
XX  OS  Conus episcopatus.
XX  PN  WO200264740-A2.
XX  PD  22-AUG-2002.
XX  PF  11-FEB-2002; 2002WO-US003887.
XX  PR  09-FEB-2001; 2001US-0267408P.
XX  PA  (COGN-) COGNETIX INC.
XX  PA  (UTAH ) UNIV UTAH RES FOUND.
XX  PI  Olivera BM, McIntosh JM, Watkins M, Jones RM, Schoenfeld RM;
XX  PI  Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
XX  DR  WPI; 2002-706921/76.
XX  DR  N-PSDB; ABX04934.
XX  PT  New cone snail conotoxin peptides, useful as a pain reliever for
XX  PT  alleviating pain in an individual suffering from pain or who is about to
XX  PT  be subjected to a pain-causing event, or for treating voltage-gated ion
XX  PT  channel disorders.
XX  PS  Claim 1; Page 235; 305pp; English.
XX  CC  This invention describes novel conotoxin peptides from the cone snail,
XX  CC  genus Conus which have analgesic activity and can act as a voltage-gated
XX  CC  ion channel modulator or a ligand-gated ion channel modulator. The
XX  CC  conotoxin peptide is useful as a pain-relieving agent for alleviating
XX  CC  pain in an individual who is either exhibiting pain or is about to be
XX  CC  subjected to a pain-causing event. The conotoxin peptide is also useful
XX  CC  for treating or preventing disorders associated with voltage-gated ion
XX  CC  channel disorders, ligand-gated ion channel disorders or receptor
XX  CC  disorders. The radiolabeled conotoxin peptide is also useful for
XX  CC  characterising a new site on these receptors or channels, and for
XX  CC  screening and identifying novel small molecules that interact with the
XX  CC  above-mentioned channels or receptors, which are monoamine transporters.
XX  CC  ABG99360-ABG99853 represent the conotoxin protein and peptides described
XX  CC  in the disclosure of the invention
XX  SQ  Sequence 64 AA;

Query Match      82.2%; Score 272; DB 5; Length 64;
Best Local Similarity 82.8%; Pred. No. 2.2e-27;
Matches 53; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY      1 MRCLPVFVILLLLLTASGPSVDAR--LTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC 58
Db      |||||
QY      59 FPCG 62
Db      |||
        61 VPCG 64

RESULT 7
ABG99606
ID  ABG99606 standard; protein; 62 AA.
XX  AC  ABG99606;
XX  DT  17-JAN-2003 (first entry)
XX  DE  Conus sp conotoxin-associated protein SEQ ID 361.
XX  KW  Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
XX  KW  ligand-gated ion channel modulator; pain-relief.
XX  OS  Conus ammiralis.
XX  PN  WO200264740-A2.
XX  PD  22-AUG-2002.
XX  PF  11-FEB-2002; 2002WO-US003887.
XX  PR  09-FEB-2001; 2001US-0267408P.
XX  PA  (COGN-) COGNETIX INC.
XX  PA  (UTAH ) UNIV UTAH RES FOUND.
XX  PI  Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
XX  PI  Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
XX  DR  WPI; 2002-706921/76.
XX  DR  N-PSDB; ABX04940.
XX  PT  New cone snail conotoxin peptides, useful as a pain reliever for
XX  PT  alleviating pain in an individual suffering from pain or who is about to
XX  PT  be subjected to a pain-causing event, or for treating voltage-gated ion
XX  PT  channel disorders.
XX  PS  Claim 1; Page 241; 305pp; English.
XX  CC  This invention describes novel conotoxin peptides from the cone snail,
XX  CC  genus Conus which have analgesic activity and can act as a voltage-gated
XX  CC  ion channel modulator or a ligand-gated ion channel modulator. The
XX  CC  conotoxin peptide is useful as a pain-relieving agent for alleviating
XX  CC  pain in an individual who is either exhibiting pain or is about to be
XX  CC  subjected to a pain-causing event. The conotoxin peptide is also useful
XX  CC  for treating or preventing disorders associated with voltage-gated ion
XX  CC  channel disorders, ligand-gated ion channel disorders or receptor
XX  CC  disorders. The radiolabeled conotoxin peptide is also useful for
XX  CC  characterising a new site on these receptors or channels, and for
XX  CC  screening and identifying novel small molecules that interact with the
XX  CC  above-mentioned channels or receptors, which are monoamine transporters.
XX  CC  ABG99360-ABG99853 represent the conotoxin protein and peptides described
XX  CC  in the disclosure of the invention
XX  SQ  Sequence 62 AA;

Query Match      80.4%; Score 266; DB 5; Length 62;
Best Local Similarity 82.3%; Pred. No. 1.2e-26;
Matches 51; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      1 MRCLPVFVILLLLLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60
Db      |||||
QY      61 CG 62
Db      |||
        61 CG 62

RESULT 8
ABG99470
ID  ABG99470 standard; protein; 64 AA.

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ligand-gated ion channel modulator; pain-relief.

Conus pennaceus.

WO200264740-A2.

22-AUG-2002.

11-FEB-2002; 2002WO-US003887.

09-FEB-2001; 2001US-0267408P.

(COGN-) COGNETIX INC.

(UTAH) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;

Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

WPI; 2002-706921/76.

N-PSDB; ABX04941.

New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.

Claim 1; Page 242; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail, genus *Conus* which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG9983 represent the conotoxin protein and peptides described in the disclosure of the invention

Sequence 64 AA;

Query Match 79.8%; Score 264; DB 5; Length 64;

Best Local Similarity 82.5%; Pred. No. 2.3e-26;

Matches 52; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

Qy 1 MRCLPVFVILLITASGPSVDAR--LKTQDVPLSSFRDNAKSTLQRHQDKVCCGYKLC 58

Db 1 MRCLPVFVILLITASGPSVDARVHLTKDGPPLSSFRDNAKSTLQRLODKSTCCGFMKC 60

Qy 59 PPC 61

Db 61 IPC 63

RESULT 11

ABG99561

ID ABG99561 standard; protein; 61 AA.

AC ABG99561;

17-JAN-2003 (first entry)

Conus sp conotoxin-associated protein SEQ ID 294.

Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;

ligand-gated ion channel modulator; pain-relief.

Conus omaria.

PN

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PD

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PA

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PA

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PI

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PI

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DR

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WO200264740-A2.

22-AUG-2002.

11-FEB-2002; 2002WO-US003887.

09-FEB-2001; 2001US-0267408P.

(COGN-) COGNETIX INC.

(UTAH) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;

Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

WPI; 2002-706921/76.

N-PSDB; ABX04918.

New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.

Claim 1; Page 218; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail, genus *Conus* which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG9983 represent the conotoxin protein and peptides described in the disclosure of the invention

Sequence 61 AA;

Query Match 76.9%; Score 254.5; DB 5; Length 61;

Best Local Similarity 85.2%; Pred. No. 3.7e-25;

Matches 52; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MRCLPVFVILLITASGPSVDARLKTQDVPLSSFRDNAKSTLQRHQDKVCCGYKLCFP 60

Db 1 MRCLPVFVILLITASGPSVDARPKAKDDVPLASFRDNAKSTLQRLODKSTCCGFMKC 59

Qy 61 C 61

Db 60 C 60

RESULT 12

ABG99612

ID ABG99612 standard; protein; 61 AA.

AC ABG99612;

17-JAN-2003 (first entry)

Conus sp conotoxin-associated protein SEQ ID 370.

Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;

ligand-gated ion channel modulator; pain-relief.

Conus omaria.

WO200264740-A2.

22-AUG-2002.

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XX

XX

PF 11-FEB-2002; 2002WO-US003887.
 PR 09-FEB-2001; 2001US-0267408P.
 XX (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX WPI; 2002-706921/76.
 DR N-PSDB; ABX04943.
 XX New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX Claim 1; Page 244; 305pp; English.
 XX This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterising a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX Sequence 61 AA;
 SQ
 Query Match 76.6%; Score 253.5; DB 5; Length 61;
 Best Local Similarity 83.6%; Pred. No. 5e-25; Indels 1; Gaps 1;
 Matches 51; Conservative 2; Mismatches 7; Indels 1; Gaps 1;
 QY 1 MRCLPVFVILLLLTASGPSVDARLKTDDVPLSSFRDNASTLQKHODKSCVCCGYKLCFP 60
 Db 1 MRCLPVFVILLLLTASGPSVDARPKAKDDVPLSSFRDNASTLQRLQDKVCCVVMC-P 59
 QY 61 C 61
 Db 60 C 60
 RESULT 13
 ABG99569
 ID ABG99569 standard; protein; 60 AA.
 XX ABG99569;
 XX 17-JAN-2003 (first entry)
 DE Conus sp conotoxin-associated protein SEQ ID 306.
 XX Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 XX ligand-gated ion channel modulator; pain-relief.
 XX Conus aulicus.
 XX WO200264740-A2.
 XX 22-AUG-2002.
 XX 11-FEB-2002; 2002WO-US003887.
 XX 09-FEB-2001; 2001US-0267408P.
 XX (COGN-) COGNETIX INC.
 XX (UTAH) UNIV UTAH RES FOUND.
 PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;

PA (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX WPI; 2002-706921/76.
 DR N-PSDB; ABX04922.
 XX New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX Claim 1; Page 222; 305pp; English.
 XX This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterising a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX Sequence 60 AA;
 SQ
 Query Match 66.5%; Score 220; DB 5; Length 60;
 Best Local Similarity 75.8%; Pred. No. 1.1e-20;
 Matches 47; Conservative 1; Mismatches 12; Indels 2; Gaps 1;
 QY 1 MRCLPVFVILLLLTASGPSVDARLKTDDVPLSSFRDNASTLQKHODKSCVCCGYKLCFP 60
 Db 1 MRCLPVFVILLLLTASGPSVDARPKTKDDVPLSSFRDNASTLQRRWNYYCTNELWC-- 58
 QY 61 CG 62
 Db 59 CG 60
 RESULT 14
 ABG99400
 ID ABG99400 standard; protein; 61 AA.
 XX ABG99400;
 XX 17-JAN-2003 (first entry)
 DE Conus sp conotoxin-associated protein SEQ ID 62.
 XX Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 XX ligand-gated ion channel modulator; pain-relief.
 XX Conus bandanus.
 XX WO200264740-A2.
 XX 22-AUG-2002.
 XX 11-FEB-2002; 2002WO-US003887.
 XX 09-FEB-2001; 2001US-0267408P.
 XX (COGN-) COGNETIX INC.
 XX (UTAH) UNIV UTAH RES FOUND.
 PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;

PI Grillley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
XX WPI; 2002-706921/76.
DR N-PSDE; ABX04847.
XX
PT New cone snail conotoxin peptides, useful as a pain reliever for
PT alleviating pain in an individual suffering from pain or who is about to
PT be subjected to a pain-causing event, or for treating voltage-gated ion
PT channel disorders.
XX
PS Claim 1; Page 130; 305pp; English.
XX
CC This invention describes novel conotoxin peptides from the cone snail,
CC genus Conus which have analgesic activity and can act as a voltage-gated
CC ion channel modulator or a ligand-gated ion channel modulator. The
CC conotoxin peptide is useful as a pain-relieving agent for alleviating
CC pain in an individual who is either exhibiting pain or is about to be
CC subjected to a pain-causing event. The conotoxin peptide is also useful
CC for treating or preventing disorders associated with voltage-gated ion
CC channel disorders, ligand-gated ion channel disorders or receptor
CC disorders. The radiolabeled conotoxin peptide is also useful for
CC characterising a new site on these receptors or channels, and for
CC screening and identifying novel small molecules that interact with the
CC above-mentioned channels or receptors, which are monoamine transporters.
CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
CC in the disclosure of the invention
XX
SQ Sequence 61 AA;

Query Match 65.3%; Score 216; DB 5; Length 61;
Best Local Similarity 68.9%; Pred. No. 3.6e-20;
Matches 42; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLITLTTASGVSVDARLKTDDVPLSSFRDNAKSTLQRHQDKSVCCGKLCFP 60
Db 1 MRCLPVLTILLITLTTASAPGVDPVLPKTDVPLSSVYDNTKSTILRGLLDRACCGKLCSP 60

Qy 61 C 61
Db 61 C 61

RESULT 15
ABG99598
ID ABG99598 standard; protein; 61 AA.
XX
AC ABG99598;
XX
DT 17-JAN-2003 (first entry)
XX
DE Conus sp conotoxin-associated protein SEQ ID 349.
XX
KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
KW ligand-gated ion channel modulator; pain-relief.
XX
OS Conus bandanus.
XX
FN WO200264740-A2.
XX
PD 22-AUG-2002.
XX
PF 11-FEB-2002; 2002WO-US003887.
XX
PR 09-FEB-2001; 2001US-0267408P.
XX
PA (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
PI Grillley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
XX
XX WPI; 2002-706921/76.
DR N-PSDB; ABX04936.
DR

XX New cone snail conotoxin peptides, useful as a pain reliever for
PT alleviating pain in an individual suffering from pain or who is about to
PT be subjected to a pain-causing event, or for treating voltage-gated ion
PT channel disorders.
XX
PS Claim 1; Page 237; 305pp; English.
XX
CC This invention describes novel conotoxin peptides from the cone snail,
CC genus Conus which have analgesic activity and can act as a voltage-gated
CC ion channel modulator or a ligand-gated ion channel modulator. The
CC conotoxin peptide is useful as a pain-relieving agent for alleviating
CC pain in an individual who is either exhibiting pain or is about to be
CC subjected to a pain-causing event. The conotoxin peptide is also useful
CC for treating or preventing disorders associated with voltage-gated ion
CC channel disorders, ligand-gated ion channel disorders or receptor
CC disorders. The radiolabeled conotoxin peptide is also useful for
CC characterising a new site on these receptors or channels, and for
CC screening and identifying novel small molecules that interact with the
CC above-mentioned channels or receptors, which are monoamine transporters.
CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
CC in the disclosure of the invention
XX
SQ Sequence 61 AA;

Query Match 65.3%; Score 216; DB 5; Length 61;
Best Local Similarity 68.9%; Pred. No. 3.6e-20;
Matches 42; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLITLTTASGVSVDARLKTDDVPLSSFRDNAKSTLQRHQDKSVCCGKLCFP 60
Db 1 MRCLPVLTILLITLTTASAPGVDPVLPKTDVPLSSVYDNTKSTILRGLLDRACCGKLCSP 60

Qy 61 C 61
Db 61 C 61

Search completed: August 10, 2004, 16:02:37
Job time : 81.4324 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:00:55 ; Search time 24.2973 Seconds
(without alignments)
131.735 Million cell updates/sec

Title: US-10-072-602B-352
Perfect score: 331
Sequence: 1 MRCLPVFVILLILLTASGPSV.....LQRHDKSVCCGYKLCFFCG 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	206	62.2	59	US-09-497-491-37	Sequence 37, Appl
2	199	60.1	60	US-09-497-491-39	Sequence 39, Appl
3	199	60.1	70	US-09-497-491-35	Sequence 35, Appl
4	180.5	54.5	62	US-09-497-491-49	Sequence 49, Appl
5	179	54.1	63	US-09-497-491-43	Sequence 43, Appl
6	169.5	51.2	62	US-09-497-491-21	Sequence 21, Appl
7	169	51.1	62	US-09-497-491-25	Sequence 25, Appl
8	167.5	50.6	64	US-09-497-491-41	Sequence 41, Appl
9	167	50.5	67	US-09-497-491-31	Sequence 31, Appl
10	166	50.2	67	US-09-497-491-33	Sequence 33, Appl
11	164	49.5	62	US-09-497-491-45	Sequence 45, Appl
12	151.5	45.8	61	US-09-497-491-23	Sequence 23, Appl
13	151.5	45.8	61	US-09-497-491-29	Sequence 29, Appl
14	148	44.7	63	US-09-497-491-47	Sequence 47, Appl
15	129.5	39.1	62	US-09-497-491-27	Sequence 27, Appl
16	59	17.8	111	US-08-456-265A-111	Sequence 111, App
17	59	17.8	111	US-08-971-217-111	Sequence 111, App
18	59	17.8	111	US-09-350-600-111	Sequence 111, App
19	59	17.8	111	US-09-906-234-111	Sequence 111, App
20	57	17.2	216	US-09-489-039A-11172	Sequence 11172, A
21	55.5	16.8	312	US-09-489-039A-11138	Sequence 11138, A
22	55.5	16.8	423	US-08-290-731C-11	Sequence 11, Appl
23	55.5	16.8	953	US-09-099-041A-8	Sequence 8, Appl
24	55.5	16.8	953	US-08-245-281-8	Sequence 8, Appl
25	55.5	16.8	953	US-09-207-359B-8	Sequence 8, Appl
26	55.5	16.8	953	US-09-340-620A-8	Sequence 8, Appl
27	55.5	16.8	953	US-09-865-364-8	Sequence 8, Appl

28	55.5	16.8	1297	2	US-08-290-731C-4	Sequence 4, Appli
29	55.5	16.8	1307	4	US-09-252-991A-20867	Sequence 20867, A
30	54.5	16.5	206	3	US-09-029-603-3	Sequence 3, Appli
31	53.5	16.2	252	4	US-09-543-681A-6220	Sequence 6220, Ap
32	53.5	16.2	383	3	US-08-857-076-105	Sequence 105, App
33	53	16.0	614	1	US-08-543-881-2	Sequence 2, Appli
34	53	16.0	614	1	US-08-291-299-2	Sequence 2, Appli
35	53	16.0	614	5	PCT-US94-00119-2	Sequence 2, Appli
36	53	16.0	614	5	PCT-US95-10579-2	Sequence 2, Appli
37	52.5	15.9	209	4	US-09-543-681A-7970	Sequence 7970, Ap
38	52.5	15.9	432	4	US-09-252-991A-24690	Sequence 24690, A
39	52.5	15.9	652	1	US-08-318-831-8	Sequence 8, Appli
40	52.5	15.9	1765	4	US-09-354-147C-2	Sequence 2, Appli
41	52.5	15.9	1765	4	US-09-354-147C-3	Sequence 3, Appli
42	52	15.7	95	1	US-08-456-265A-110	Sequence 110, App
43	52	15.7	95	2	US-08-971-217-110	Sequence 110, App
44	52	15.7	95	3	US-09-350-600-110	Sequence 110, App
45	52	15.7	95	4	US-09-906-234-110	Sequence 110, App

ALIGNMENTS

RESULT 1
US-09-497-491-37
; Sequence 37, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Conus marmoreus
US-09-497-491-37

Query Match 62.2%; Score 206; DB 4; Length 59;
Best Local Similarity 70.7%; Pred. No. 4.2e-20;
Matches 41; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLILLTASGPSVDARLKTDDVPLSSFRDNAXSTLQRHDKSVCCGYKLC 58
Db 1 MRCLPVFVILLILLTASGPSVDARPKTKDDMPPLASFDNAXRILQLQDRNACCIVRQC 58

RESULT 2
US-09-497-491-39
; Sequence 39, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491

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; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Conus marmoreus
US-09-497-491-39

Query Match      60.1%; Score 199; DB 4; Length 60;
Best Local Similarity 75.5%; Pred. No. 3.6e-19;
Matches 40; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLTASGSPVDARLTKDDVPLSSFRDNASTLQRHODKSVCC 53
    |||||
Db 1 MRCLPVFVILLTASGSPVDARPKTKDDMPPLASFHDNAKRIQLQDRNGCC 53
    |||||

RESULT 3
US-09-497-491-35
; Sequence 35, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus marmoreus
US-09-497-491-35

Query Match      60.1%; Score 199; DB 4; Length 70;
Best Local Similarity 75.5%; Pred. No. 4.4e-19;
Matches 40; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLTASGSPVDARLTKDDVPLSSFRDNASTLQRHODKSVCC 53
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Db 1 MRCLPVFVILLTASGSPVDARPKTKDDMPPLASFHDNAKRIQLQDRNGCC 53
    |||||

RESULT 4
US-09-497-491-49
; Sequence 49, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
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; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Conus gloriamaris
US-09-497-491-49

Query Match      54.5%; Score 180.5; DB 4; Length 62;
Best Local Similarity 71.7%; Pred. No. 1.1e-16;
Matches 38; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MRCLPVFVILLTASGSPVDARLTKDDVPLSSFRDNASTLQRHODKSVCC 53
    |||||
Db 1 MRCLPVFVILLTASGSPVDARPKTKDDVPLAPLHDNIRSTLQTLR-KKVC 52
    |||||

RESULT 5
US-09-497-491-43
; Sequence 43, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Conus characteristicus
US-09-497-491-43

Query Match      54.1%; Score 179; DB 4; Length 63;
Best Local Similarity 61.0%; Pred. No. 1.7e-16;
Matches 36; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLTASGSPVDARLTKDDVPLSSFRDNASTLQRHODKSVCC 59
    |||||
Db 1 MRCLPVFVILLTASGSPVDARPKTKDYDAPLTSLHDNAKGIQEHWNKRCCPNKPCCF 59
    |||||

RESULT 6
US-09-497-491-21
; Sequence 21, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
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; LENGTH: 62
; TYPE: PRT
; ORGANISM: Conus textile
US-09-497-491-21

Query Match      51.2%; Score 169.5; DB 4; Length 62;
Best Local Similarity 63.8%; Pred. No. 3e-15;
Matches 37; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

QY 1 MRCLPVFVILLILLTASGPSVDARLKTDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC 58
Db 1 MCCLPVFVILLILLTASGPSVDAPQTKDDVPLPLHDNAKSALQ-HLNQRCCQTFYC 57

RESULT 7
US-09-497-491-25
; Sequence 25, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Conus quercinus
US-09-497-491-25

Query Match      51.1%; Score 169; DB 4; Length 62;
Best Local Similarity 60.3%; Pred. No. 3.5e-15;
Matches 35; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 MRCLPVFVILLILLTASGPSVDARLKTDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC 58
Db 1 MRCVPFVILLILLSPSAPSDAHPEMTKDDVPOASHDDAKRTLOVPWMKRGCCARLTC 58

RESULT 8
US-09-497-491-41
; Sequence 41, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Conus characteristicus

US-09-497-491-41
Query Match      50.6%; Score 167.5; DB 4; Length 64;
Best Local Similarity 61.4%; Pred. No. 5.7e-15;
Matches 35; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

QY 1 MRCLPVFVILLILLTASGPSVDARLKTDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC 57
Db 1 MRCLPVFVILLILLTASGPSVDAPQTKYNAPLTSLHDNAKGLQEHWNKR-CCPRRL 56

RESULT 9
US-09-497-491-31
; Sequence 31, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus textile
US-09-497-491-31

Query Match      50.5%; Score 167; DB 4; Length 67;
Best Local Similarity 62.3%; Pred. No. 7.1e-15;
Matches 33; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 MRCLPVFVILLILLTASGPSVDARLKTDDVPLSSFRDNAKSTLQRHQDKSVCC 53
Db 1 MRCFPVFIILLILLTASAPCFDARTKDDDDVPLSLRDLNKKRTIRTLNIRECC 53

RESULT 10
US-09-497-491-33
; Sequence 33, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus textile
US-09-497-491-33

Query Match      50.2%; Score 166; DB 4; Length 67;
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Best Local Similarity 62.3%; Pred. No. 9.6e-15;
Matches 33; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLITLTSAGPSVDARLTKDDVPLSSFRDNAKSTLQRHQKSVCC 53
Db 1 MRCLPVFVILLITLTSAGPSVDARLTKDDVPLSSFRDNAKSTLQRHQKSVCC 53

RESULT 11
US-09-497-491-45

; Sequence 45, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Conus quercinus
US-09-497-491-45

Query Match 49.5%; Score 164; DB 4; Length 62;
Best Local Similarity 58.6%; Pred. No. 1.6e-14;
Matches 34; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLITLTSAGPSVDARLTKDDVPLSSFRDNAKSTLQRHQKSVCCGYKLC 58
Db 1 MRCLPVFVILLITLTSAGPSVDARLTKDDVPLSSFRDNAKSTLQRHQKSVCCGYKLC 58

RESULT 12
US-09-497-491-23

; Sequence 23, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Conus geographus
US-09-497-491-23

Query Match 45.8%; Score 151.5; DB 4; Length 61;
Best Local Similarity 58.3%; Pred. No. 7e-13;
Matches 35; Conservative 4; Mismatches 14; Indels 7; Gaps 2;

Qy 1 MRCLPVFVILLITLTSAGPSVDARLTKDDVPLSSFRD--NAKSTLQRHQ-----DKSVCC 53
Db 1 MRCLPVFVILLITLTSAGPSVDALPKTRDDVPLASHFGGYNARRILQRRQGWCKENIACC 60

RESULT 13

US-09-497-491-29

; Sequence 29, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Conus geographus
US-09-497-491-29

Query Match 45.8%; Score 151.5; DB 4; Length 61;
Best Local Similarity 58.3%; Pred. No. 7e-13;
Matches 35; Conservative 4; Mismatches 14; Indels 7; Gaps 2;

Qy 1 MRCLPVFVILLITLTSAGPSVDARLTKDDVPLSSFRD--NAKSTLQRHQ-----DKSVCC 53
Db 1 MRCLPVFVILLITLTSAGPSVDALPKTRDDVPLASHFGGYNARRILQRRQGWCKENIACC 60

RESULT 14

US-09-497-491-47

; Sequence 47, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Conus gloriamaris
US-09-497-491-47

Query Match 44.7%; Score 148; DB 4; Length 63;
Best Local Similarity 58.5%; Pred. No. 2.1e-12;
Matches 31; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLITLTSAGPSVDARLTKDDVPLSSFRDNAKSTLQRHQKSVCC 53
Db 1 MRCLPVFVILLITLTSAGPSVDALPKTRDDVPLASHFGGYNARRILQRRQGWCKENIACC 60


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RESULT 15
US-09-497-491-27
; Sequence 27, Application US/09497491
; Patent No. 6630573
; GENERAL INFORMATION:
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hooper, David
; APPLICANT: Jacobsen, Richard
; APPLICANT: Steele, Doug
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Tau-Conotoxin Peptides
; FILE REFERENCE: Tau-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/497,491
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: US 60/118,642
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Conus imperialis
US-09-497-491-27

Query Match      39.1%; Score 129.5; DB 4; Length 62;
Best Local Similarity 50.8%; Pred. No. 5.8e-10;
Matches 32; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

QY      1 MRCLPVFVILLILLTASGPSVDARLKTDDVPLSSFRDPAKSTLQRHQDKSVCCGYKL-CF 59
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Db      1 MYCLPVFILLILLISSAESTPPQPRNKORVHLISLLDNHKKQLQR--DWNSSCCGKNPGCC 58
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY      60 PCG 62
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Db      59 PWG 61

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:04:26 ; Search time 67.8649 Seconds
(without alignments)
286.575 Million cell updates/sec

Title: US-10-072-602B-352
Perfect score: 331

Sequence: 1 MRCLPVFVILLITLTSAGPSV.....LQRHODKSVCCGYKLCFPCG 62

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Searched: 1291235 seqs, 313682936 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:
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3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	298	90.0	62	14	US-10-072-602B-339
3	286	86.4	62	14	US-10-072-602B-336
4	281	84.9	62	14	US-10-072-602B-229
5	281	84.9	62	14	US-10-072-602B-358
6	276	83.4	64	14	US-10-072-602B-342
7	266	80.4	62	14	US-10-072-602B-361
8	264	79.8	64	14	US-10-072-602B-162
9	264	79.8	64	14	US-10-072-602B-333
10	264	79.8	64	14	US-10-072-602B-364
11	254.5	76.9	61	14	US-10-072-602B-294
12	253.5	76.6	61	14	US-10-072-602B-370
13	220	66.5	60	14	US-10-072-602B-306
14	216	65.3	61	14	US-10-072-602B-62
15	216	65.3	61	14	US-10-072-602B-349

16 211.5 63.9 61 14 US-10-072-602B-279 Sequence 279, App
17 208 62.8 61 14 US-10-072-602B-309 Sequence 309, App
18 201.5 60.9 61 14 US-10-072-602B-288 Sequence 288, App
19 200 60.4 58 14 US-10-072-602B-291 Sequence 291, App
20 192 58.0 61 14 US-10-072-602B-330 Sequence 330, App
21 191 57.7 61 14 US-10-072-602B-345 Sequence 345, App
22 188 56.8 63 14 US-10-072-602B-285 Sequence 285, App
23 180 54.4 59 14 US-10-072-602B-297 Sequence 297, App
24 176 53.2 60 14 US-10-072-602B-303 Sequence 303, App
25 175 52.9 59 14 US-10-072-602B-300 Sequence 300, App
26 163.5 49.4 64 14 US-10-072-602B-276 Sequence 276, App
27 130 39.3 61 14 US-10-072-602B-282 Sequence 282, App
28 79 23.9 12 14 US-10-072-602B-534 Sequence 534, App
29 69 20.8 13 14 US-10-072-602B-529 Sequence 529, App
30 69 20.8 16 14 US-10-072-602B-355 Sequence 355, App
31 69 20.8 300 12 US-10-282-122A-53389 Sequence 53389, A
32 64.5 19.5 1010 16 US-10-437-963-104971 Sequence 104971,
33 63.5 19.2 105 16 US-10-437-963-177312 Sequence 177312,
34 63 19.0 11 14 US-10-072-602B-524 Sequence 524, App
35 63 19.0 11 14 US-10-072-602B-533 Sequence 533, App
36 63 19.0 12 14 US-10-072-602B-527 Sequence 527, App
37 63 19.0 12 14 US-10-072-602B-528 Sequence 528, App
38 63 19.0 13 14 US-10-072-602B-525 Sequence 525, App
39 63 19.0 13 14 US-10-072-602B-526 Sequence 526, App
40 63 19.0 13 14 US-10-072-602B-535 Sequence 535, App
41 63 19.0 13 14 US-10-072-602B-538 Sequence 538, App
42 63 19.0 423 12 US-10-282-122A-70228 Sequence 70228, A
43 62 18.7 12 14 US-10-072-602B-353 Sequence 353, App
44 62 18.7 1044 12 US-10-282-122A-53474 Sequence 53474, A
45 60.5 18.3 79 16 US-10-437-963-131646 Sequence 131646,

ALIGNMENTS

RESULT 1

US-10-072-602B-352
; Sequence 352, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Balomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 352
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Conus aulicus
US-10-072-602B-352

Query Match 100.0%; Score 331; DB 14; Length 62;

Best Local Similarity 100.0%; Pred. No. 3.1e-33;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRCLPVFVILLITLTSAGPSVDARLKTDDVPLSFRNNAKSTLQRHODKSVCCGYKLCFPCG 60

Db 1 MRCLPVFVILLITLTSAGPSVDARLKTDDVPLSFRNNAKSTLQRHODKSVCCGYKLCFPCG 60

QY	61	CG	62
Db	61	CG <td>62</td>	62
<p>RESULT 2</p> <p>US-10-072-602B-339</p> <p>Sequence 339, Application US/10072602B</p> <p>Publication No. US20030109670A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: University of Utah Research Foundation</p> <p>APPLICANT: Cognetix, Inc.</p> <p>APPLICANT: Olivera, Baldomero M.</p> <p>APPLICANT: McIntosh, J, Michael</p> <p>APPLICANT: Watkins, Maren</p> <p>APPLICANT: Garrett, James E.</p> <p>APPLICANT: Cruz, Lourdes J.</p> <p>APPLICANT: Grilley, Michelle</p> <p>APPLICANT: Schoenfeld, Robert M.</p> <p>APPLICANT: Walker, Craig</p> <p>APPLICANT: Shetty, Reshma</p> <p>APPLICANT: Jones, Robert M.</p> <p>TITLE OF INVENTION: Cone Snail Peptides</p> <p>FILE REFERENCE: 2314-249</p> <p>CURRENT APPLICATION NUMBER: US/10/072,602B</p> <p>PRIOR FILING DATE: 2002-02-11</p> <p>PRIOR APPLICATION NUMBER: US 60/267,408</p> <p>PRIOR FILING DATE: 2001-02-09</p> <p>NUMBER OF SEQ ID NOS: 638</p> <p>SOFTWARE: PatentIn version 3.0</p> <p>SEQ ID NO 339</p> <p>LENGTH: 62</p> <p>TYPE: PRT</p> <p>ORGANISM: <i>Conus pennaceus</i></p> <p>US-10-072-602B-339</p>			
QY	61	CG	62
Db	61	CG	62
<p>Query Match 90.0%; Score 298; DB 14; Length 62;</p> <p>Best Local Similarity 88.7%; Pred. No. 3.7e-29;</p> <p>Matches 55; Conservative 4; Mismatches 3; Indels 0; Gaps 0;</p>			
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Db	1	MRCPLPVFVILLITAGSPVDARLTKDDVPLSSFRDNAKSTLQRHDKSVCCGKLCFP	60
QY	61	CG	62
Db	61	CG	62
<p>RESULT 3</p> <p>US-10-072-602B-336</p> <p>Sequence 336, Application US/10072602B</p> <p>Publication No. US20030109670A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: University of Utah Research Foundation</p> <p>APPLICANT: Cognetix, Inc.</p> <p>APPLICANT: Olivera, Baldomero M.</p> <p>APPLICANT: McIntosh, J, Michael</p> <p>APPLICANT: Watkins, Maren</p> <p>APPLICANT: Garrett, James E.</p> <p>APPLICANT: Cruz, Lourdes J.</p> <p>APPLICANT: Grilley, Michelle</p> <p>APPLICANT: Schoenfeld, Robert M.</p> <p>APPLICANT: Walker, Craig</p> <p>APPLICANT: Shetty, Reshma</p> <p>APPLICANT: Jones, Robert M.</p> <p>TITLE OF INVENTION: Cone Snail Peptides</p> <p>FILE REFERENCE: 2314-249</p> <p>CURRENT APPLICATION NUMBER: US/10/072,602B</p> <p>PRIOR FILING DATE: 2002-02-11</p> <p>PRIOR APPLICATION NUMBER: US 60/267,408</p> <p>PRIOR FILING DATE: 2001-02-09</p>			


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; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 162
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Conus pennaceus
US-10-072-602B-162

Query Match          79.8%; Score 264; DB 14; Length 64;
Best Local Similarity 82.5%; Pred. No. 6e-25;
Matches 52; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

Qy 1 MRCLPVFVILLTASGPSVDAR--LTKYDVPVLSFRDNASTLQRHQDKSVCCGYKLC 58
Db 1 MRCLPVFVILLTASGPSVDARVDAKVLTKGDPGLSPFRDNASTLQRHQDKSVCCGYKLC 60

Qy 59 FPC 61
Db 61 IPC 63

RESULT 9
US-10-072-602B-333
; Sequence 333, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 333
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Conus pennaceus
US-10-072-602B-333

Query Match          79.8%; Score 264; DB 14; Length 64;
Best Local Similarity 82.5%; Pred. No. 6e-25;
Matches 52; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

Qy 1 MRCLPVFVILLTASGPSVDAR--LTKYDVPVLSFRDNASTLQRHQDKSVCCGYKLC 58
Db 1 MRCLPVFVILLTASGPSVDARVDAKVLTKGDPGLSPFRDNASTLQRHQDKSVCCGYKLC 60

Qy 59 FPC 61
Db 61 IPC 63

RESULT 10
US-10-072-602B-364
; Sequence 364, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
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```
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 364
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Conus pennaceus
US-10-072-602B-364

Query Match          79.8%; Score 264; DB 14; Length 64;
Best Local Similarity 82.5%; Pred. No. 6e-25;
Matches 52; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

Qy 1 MRCLPVFVILLTASGPSVDAR--LTKYDVPVLSFRDNASTLQRHQDKSVCCGYKLC 58
Db 1 MRCLPVFVILLTASGPSVDARVDAKVLTKGDPGLSPFRDNASTLQRHQDKSVCCGYKLC 60

Qy 59 FPC 61
Db 61 IPC 63

RESULT 11
US-10-072-602B-294
; Sequence 294, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 294
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Conus omaria
US-10-072-602B-294

Query Match          76.9%; Score 254.5; DB 14; Length 61;
Best Local Similarity 85.2%; Pred. No. 8.4e-24;
Matches 52; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MRCLPVFVILLTASGPSVDARLTKYDVPVLSFRDNASTLQRHQDKSVCCGYKLC 60
```

Db 1 MRCLPVFVILLTASAPSDARPKAKDDVPLASFSDNAKSTLQRLQDKRVCCGYKF-FC 59
Qy 61 C 61
Db 60 C 60

RESULT 12
US-10-072-602B-370
; Sequence 370, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 370
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Conus omaria
US-10-072-602B-370

Query Match 76.6%; Score 253.5; DB 14; Length 61;
Best Local Similarity 83.6%; Pred. No. 1.1e-23;
Matches 51; Conservative 2; Mismatches 7; Indels 1; Gaps 1;
Qy 1 MRCLPVFVILLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHODKSVCCGYKLCFP 60
Db 1 MRCLPVFVILLTASAPSDARPKAKDDVPLSSFRDNAKSTLQRLQDKRVCCYVRMC-P 59
Qy 61 C 61
Db 60 C 60

RESULT 13
US-10-072-602B-306
; Sequence 306, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11

; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 306
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Conus aulicus
US-10-072-602B-306

Query Match 66.5%; Score 220; DB 14; Length 60;
Best Local Similarity 75.8%; Pred. No. 1.5e-19;
Matches 47; Conservative 1; Mismatches 12; Indels 2; Gaps 1;
Qy 1 MRCLPVFVILLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHODKSVCCGYKLCFP 60
Db 1 MRCLPVFVILLTASGPSVDARPKTKDDVPLSSFRDNAKSTLQRRWNNYCTNELWC-- 58
Qy 61 CG 62
Db 59 CG 60

RESULT 14
US-10-072-602B-62
; Sequence 62, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Conus bandanus
US-10-072-602B-62

Query Match 65.3%; Score 216; DB 14; Length 61;
Best Local Similarity 68.9%; Pred. No. 4.7e-19;
Matches 42; Conservative 3; Mismatches 16; Indels 0; Gaps 0;
Qy 1 MRCLPVFVILLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHODKSVCCGYKLCFP 60
Db 1 MRCLPVFVILLTASAPSGVDVLPKTEDDVPSSVYDNTKSLKGLDKRACCGYKLCSP 60
Qy 61 C 61
Db 61 C 61

RESULT 15
US-10-072-602B-349
; Sequence 349, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 349
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Conus bandanus
US-10-072-602B-349

Query Match 65.3%; Score 216; DB 14; Length 61;
Best Local Similarity 68.9%; Pred. No. 4.7e-19;
Matches 42; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MRCLPVPVILLILTLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCFP 60
Db 1 MRCLPVLILLILLTLTASAFGVDVLPKTEDDVPLSSVYDNTKSLRGLLDKACCGYKLCSP 60

Qy 61 C 61
Db 61 C 61

Search completed: August 10, 2004, 16:13:54
Job time : 68.8649 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:00:00 ; Search time 19.2703 Seconds
(without alignments)
309.486 Million cell updates/sec

Title: US-10-072-602b-352

Perfect score: 331

Sequence: 1 MRCLPVFVILLLLTASGPSV.....LQRHQDKSVCCGYKLCRPGC 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	56.8	63	2 F59147	conotoxin P5.1 pre
2	180.5	54.5	62	2 D59147	conotoxin Gm5.2 pr
3	169.5	51.2	62	2 B59147	conotoxin Tx5.1 pr
4	167	50.5	67	2 E59147	conotoxin Tx5.2 pr
5	148	44.7	63	2 C59147	conotoxin Gm5.1 pr
6	129.5	39.1	62	2 G59147	conotoxin Im5.1 pr
7	63	19.0	423	2 B89784	hypothetical prote
8	62	18.7	715	2 S77439	hypothetical prote
9	61	18.4	315	1 HNVZVT	hemagglutinin prec
10	60	18.1	389	2 H90413	conserved hypothet
11	59.5	18.0	457	2 T18347	gag protein homolo
12	59.5	18.0	2148	1 A56081	insulin receptor -
13	59	17.8	111	2 T03701	SAR8.2e protein, T
14	58	17.5	551	2 A10393	oligopeptide ABC t
15	58	17.5	929	2 A32495	rep-1 protein, for
16	58	17.5	1126	2 JC4019	DNA mismatch repai
17	58	17.5	1131	2 T38744	hypothetical prote
18	58	17.5	1992	1 S02771	myosin heavy chain
19	57.5	17.4	188	2 T48200	hypothetical prote
20	57.5	17.4	541	2 T47290	hypothetical prote
21	57.5	17.4	772	2 H84605	hypothetical prote
22	57.5	17.4	802	1 A26343	phosphoribosylamin
23	57	17.2	323	2 I64240	hypothetical prote
24	57	17.2	453	2 B97738	outer membrane pro
25	57	17.2	662	2 A29900	fasciclin I precu
26	56	16.9	369	2 S74983	hypothetical prote
27	56	16.9	633	2 T27499	hypothetical prote
28	56	16.9	975	2 T29908	hypothetical prote
29	55.5	16.8	165	2 H84634	hypothetical prote

30 55.5 16.8 518 2 T45765 hypothetical prote
31 55.5 16.8 907 1 A57429 aldehyde oxidase (

32 55.5 16.8 1287 2 S55954 viral mRNA transla
33 55.5 16.8 1297 2 S25714 son-of-sevenless-2
34 55 16.6 170 1 NWMU2 2S albumin 2 precu
35 55 16.6 185 2 S51803 vomeronasal secret
36 55 16.6 281 2 AF0505 probable exported
37 55 16.6 311 2 G81402 oxidoreductase Cj0
38 55 16.6 467 1 Q2AGAT indoleacetamide hy
39 55 16.6 633 2 T39352 hypothetical prote
40 55 16.6 789 2 S73357 topoisomerase IV c
41 55 16.6 914 2 S18942 hypothetical prote
42 54.5 16.5 162 2 T08013 hypothetical prote
43 54.5 16.5 1010 2 T13167 2S seed storage pr
44 54.5 16.5 1735 2 A57607 Lola-like protein
45 54 16.3 260 2 H84188 Munc13-1 - rat
hypothetical prote

ALIGNMENTS

RESULT 1

F59147

conotoxin P5.1 precursor - cone shell (Conus purpurascens)

N:Contains: conotoxin p5a

C:Species: Conus purpurascens (purple cone)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-May-2000

C/Accession: F59147

R:Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty

J. Biol. Chem. 274, 30664-30671, 1999

A:Title: The T-superfamily of conotoxins.

A:Reference number: A59147; MUID:99452958; PMID:10521453

A/Accession: F59147

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA; protein

A:Residues: 1-63 <WAL>

A/Cross-references: GB:AF167168; NID:g6103614; PIDN:AAF03688.1; PID:g6103615

A>Note: submitted to GenBank, July 1999

C:Superfamily: unassigned conotoxins

C:Keywords: amidated carboxyl end; toxin; venom

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-50/Domain: propeptide #status predicted <PRO>

F:51-62/Product: conotoxin p5a #status experimental <MAT>

F:52-59,53-60/Disulfide bonds: #status experimental

F:62/Modified site: amidated carboxyl end (Leu) (amide in mature form from following gly

Query Match

Best Local Similarity 56.8%; Score 188; DB 2; Length 63;

Matches 38; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLLLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHQDKSVCC 53

Db 1 MRCLPVFVILLLLTASGPSVDARLTKDDVPLSSFRDNAKSTLQRHQDKSVCC 53

RESULT 2

D59147

conotoxin Gm5.2 precursor - cone shell (Conus gloriamaris)

C:Species: Conus gloriamaris (glory-of-the-sea cone)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-May-2000

C/Accession: D59147

R:Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty

J. Biol. Chem. 274, 30664-30671, 1999

A:Title: The T-superfamily of conotoxins.

A:Reference number: A59147; MUID:99452958; PMID:10521453

A/Accession: D59147

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-62 <WAL>

A/Cross-references: GB:AF167166; NID:g6103610; PIDN:AAF03686.1; PID:g6103611

A>Note: submitted to GenBank, July 1999

C:Superfamily: unassigned conotoxins

C:Keywords: amidated carboxyl end; toxin; venom

Proc. Natl. Acad. Sci. U.S.A. 96, 5758-5763, 1999
A>Title: A conotoxin from *Conus textile* with unusual posttranslational modifications reduced toxicity
A/Reference number: A59044; MUID: 99254114; PMID: 10318957
A/Accession: A59044
A/Status: preliminary
A/Molecule type: protein

F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-45/Domain: propeptide #status predicted <PRO>
 F:46-60/Product: conotoxin im5 #status predicted <MAT>
 F:50-57,51-59/Disulfide bonds: #status predicted
 F:60/Modified site: amidated carboxyl end (Trp) (amide in mature form from following gly

Query Match 39.1%; Score 129.5; DB 2; Length 62;
 Best Local Similarity 50.8%; Pred. No. 1.3e-08;
 Matches 32; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

Qy 1 MRCLPVFVILLTASGSDVRLTKDDVPLSSFRDNKSTLQRHDKSVCCGYKL-CF 59
 Db 1 MYCLPVFIILLTASAPSTPPQPRNKRKHVLSLLDNHKKILQR--DWNSSCCGNPGCC 58

Qy 60 PGC 62
 Db 59 FWG 61

RESULT 7
 B99784
 hypothetical protein SA0207 [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: B99784
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaishi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: B99758; UID:21311952; PMID:11418146

A:Accession: B99784

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-423 <KUR>

A:Cross-references: GB:BA00018; PID:gl3700130; PIDN:BA041429.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA0207

C:Superfamily: maltose-binding protein

Query Match 19.0%; Score 63; DB 2; Length 423;
 Best Local Similarity 31.7%; Pred. No. 8.6;
 Matches 13; Conservative 15; Mismatches 7; Indels 6; Gaps 2;

Qy 1 MRCLPVFVILLTASGSDVRLTKDDVPLSSFRDNK 40
 Db 5 LKCLTAVVLLIVTACGPN-----RSKEDIDKALNKD 40

RESULT 8
 S77439
 hypothetical protein slr135 - Synecocystis sp. (strain PCC 6803)
 C:Species: Synecocystis sp.
 A:Variety: PCC 6803
 C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C:Accession: S77439

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis

A:Reference number: S74322; UID:97061201; PMID:8905231

A:Accession: S77439

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-715 <KAN>

A:Cross-references: EMBL:D90905; GB:AB001339; NID:gl652360; PIDN:BA017286.1; PID:dl01801

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 18.7%; Score 62; DB 2; Length 715;
 Best Local Similarity 28.0%; Pred. No. 18;
 Matches 14; Conservative 7; Mismatches 21; Indels 8; Gaps 1;

Qy 20 VDARLTKDDVPLSFRD-----NAKSTLQRHDKSVCCGYKLCPFC 61
 Db 577 IDVKSTDYFLKISSFOGHILYSIFNYFQLLYHNEHKSCIGYACFTC 626

RESULT 9

HNWZVT

hemagglutinin precursor - vaccinia virus (strain Tiantan)

C:Species: vaccinia virus

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jul-1999

C:Accession: J10108

R:Jin, D.; Li, Z.; Jin, Q.; Yuwen, H.; Hou, Y.

J. Exp. Med. 170, 571-576, 1989

A:Title: Vaccinia virus hemagglutinin. A novel member of the immunoglobulin superfamily.

A:Reference number: J10108; UID:89328331; PMID:2754392

A:Accession: J10108

A:Molecule type: mRNA

A:Residues: 1-315 <JIN>

A:Cross-references: GB:X15709; GB:M57773; NID:g61313; PIDN:CAA33740.1; PID:g61314

C:Superfamily: vaccinia virus hemagglutinin; immunoglobulin homology

C:Keywords: glycoprotein; hemagglutinin; late protein; transmembrane protein

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-315/Product: hemagglutinin #status predicted <MAT>

F:27-105/Domain: immunoglobulin homology <IMM>

F:280-302/Domain: transmembrane #status predicted <TM>

F:303-315/Domain: intracellular #status predicted <INT>

F:37,69,112,161,254/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 18.4%; Score 61; DB 1; Length 315;

Matches 15; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLTASGSDVRLTKDDVPLSSFRDN 38

Db 1 MARLPILLLLISLVSTPSPQTSKKGIDATLSGNRN 38

RESULT 10

H90413

conserved hypothetical protein [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: H90413

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.

arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: H90413

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-389 <KUR>

A:Cross-references: GB:AE006641; NID:gl3815727; PIDN:AAK42567.1; GSPDB:GN00155

C:Genetics:

A:Gene: SS02423

Query Match

Best Local Similarity 18.1%; Score 60; DB 2; Length 389;

Matches 15; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 18 PSVDARLTKDDVPLSSFRDNKSTLQRHDK 49

Db 138 PTVSDRDSIKDVPFSSFPVKSYLEVQDK 169

RESULT 11

T18347

gag protein homolog, truncated - rice blast fungus magnaporthe gypsy retrotransposon

C:Species: Magnaporthe grisea (rice blast fungus)

C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000

C:Accession: T18347

Mol. Cell. Biol. 9, 3058-3072, 1989
A;Title: Dual bidirectional promoters at the mouse dhfr locus: cloning and characterization
A;Reference number: A32495; MUID:89384567; PMID:2674679
A;Accession: A32495
A;Molecule type: mRNA
A;Residues: 1-929 <LIN>
A;Cross-references: GB:M24919; GB:J04244
C;Genetics:
A;Gene: rep-1
C;Keywords: DNA binding

Query Match 17.5%; Score 58; DB 2; Length 929;
Best Local Similarity 32.1%; Pred. NO. 71;
Matches 18; Conservative 5; Mismatches 17; Indels 16; Gaps 3;

QY 17 GPSVDARLKTDDVPLSPFDNAKSTL-----QRHODKSV--CGYKLCF 59
Db 164 GPCPEVFQKTSCKP---FNKRSKVYTPLEQLYLDMMKQHKDAVLCVECGYKYRF 216

Search completed: August 10, 2004, 16:04:56
Job time : 19.2703 secs

blank sheet

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OM protein - protein search, using sw model

Run on: August 10, 2004, 15:56:10 ; Search time 13.4054 seconds
(without alignments)
240.824 Million cell updates/sec

Title: US-10-072-602B-352

Perfect score: 331

Sequence: 1 MCCLPVFVILLITAGSPV.....LQRHQDKSVCCGYKLCFPG 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	57.7	61	1	CXL2 CONMR
2	188	56.8	63	1	CXSA CONFU
3	180.5	54.5	62	1	CX52 CONGL
4	169.5	51.2	62	1	CX51 CONTE
5	167	50.5	67	1	CXET CONTE
6	148	44.7	63	1	CX51 CONGL
7	129.5	39.1	62	1	CX51 CONIM
8	68	20.5	11	1	CXL1 CONMR
9	68	20.5	13	1	CXL4 CONMR
10	61	18.4	315	1	HEMA VACCT
11	59	17.8	313	1	SPY2 CHICK
12	58	17.5	1091	1	MSH3 MOUSE
13	58	17.5	1131	1	YANC SCHPO
14	58	17.5	1969	1	MYSA CAEEL
15	57.5	17.4	802	1	PUR2 YEAST
16	57	17.2	323	1	Y370 MYCCE
17	57	17.2	662	1	FAS1 SCHAM
18	56.5	17.1	650	1	APPI HUMAN
19	56	16.9	369	1	YF00 SYNY3
20	55.5	16.8	907	1	MAR_DESGI
21	55.5	16.8	953	1	CAR4 HUMAN
22	55.5	16.8	1287	1	SK12 YEAST
23	55.5	16.8	1297	1	SOS2 MOUSE
24	55	16.6	170	1	2SS2 ARATH
25	55	16.6	185	1	VNS2 MOUSE
26	55	16.6	467	1	HYIN AGRTU
27	55	16.6	789	1	PARC MYCPN
28	55	16.6	3726	1	ABF1 MOUSE
29	54.5	16.5	266	1	RP0D METMA
30	54	16.3	12	1	CXL3 CONMR
31	54	16.3	262	1	FBOL_BONMO
32	54	16.3	345	1	CLT2 PIG
33	54	16.3	708	1	CAO2_CANTR

34	54	16.3	1316	1	RPOC MYCTU
35	54	16.3	2410	1	POLI BAYMJ
36	53.5	16.2	287	1	CAPB YEAST
37	53.5	16.2	545	1	THSB_ARCFU
38	53.5	16.2	630	1	S6A4 MOUSE
39	53.5	16.2	2146	1	INSR_DROME
40	53	16.0	212	1	URED_BACPA
41	53	16.0	245	1	IEO NPVOP
42	53	16.0	499	1	GUNI_BACSU
43	53	16.0	614	1	S6AC_HUMAN
44	53	16.0	1021	1	PSKE_DAUCA
45	53	16.0	5127	1	RY44_DROME

ALIGNMENTS

RESULT 1					
CXL2_CONMR					
ID	CXL2_CONMR	STANDARD;	PRT;	61	AA.
AC	P58808;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Lambda-conotoxin CMVIB precursor (Chi-conotoxin Mria) (Chi-Mria) (mr10a).				
DE	Conus marmoreus (Marble cone).				
OS	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;				
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;				
OC	Neogastropoda; Conoidea; Conidae; Conus.				
OX	NCBI_TaxID=42752;				
RN	[1]				
RP	SEQUENCE FROM N.A., SEQUENCE OF 49-61, SYNTHESIS, AND MASS SPECTROMETRY.				
RC	TISSUE=Venom, and Venom duct;				
RX	MEDLINE=20490660; PubMed=10900201;				
RA	McIntosh J.M., Corpuz G.O., Layer R.T., Garrett J.E., Wagstaff J.D.,				
RA	Bulaj G., Vyazovkina A., Yoshikami D., Cruz L.J., Olivera B.M.;				
RT	"Isolation and characterization of a novel conus peptide with apparent antinociceptive activity";				
RT	J. Biol. Chem. 275:32391-32397(2000).				
RL	[2]				
RP	SEQUENCE OF 49-61, AND MASS SPECTROMETRY.				
RC	TISSUE=Venom;				
RX	MEDLINE=20564325; PubMed=10988292;				
RA	Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,				
RA	Seow K.T., Bay B.-H.;				
RT	"Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of Conus marmoreus.";				
RL	[3]				
RP	SEQUENCE OF 49-61, SYNTHESIS, MASS SPECTROMETRY, AND STRUCTURE BY NMR.				
RC	TISSUE=Venom;				
RX	MEDLINE=21419681; PubMed=11528421;				
RA	Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,				
RA	Atkins A., Falant E., Craik D.J., Adams D.J., Alewood P.F.,				
RA	Lewis R.J.;				
RT	"Two new classes of conopeptides inhibit the alpha-adrenoceptor and noradrenaline transporter.";				
RL	Nat. Neurosci. 4:902-907(2001).				
CC	- FUNCTION: Inhibits the neuronal noradrenaline transporter.				
CC	- SUBCELLULAR LOCATION: Secreted.				
CC	- TISSUE SPECIFICITY: Expressed by the venom duct.				
CC	- PTM: Exists in two forms, due to cis-trans isomerization at His-59-Hyp-60.				
CC	- MASS SPECTROMETRY: MW=1408.5; METHOD=Electrospray.				
CC	- SIMILARITY: Belongs to the chi/lambda-conotoxin family.				
DR	InterPro: IPR004214; Conotoxin.				
KW	Pfam: PF02950; Conotoxin; 1				
KW	Neurotoxin; Toxin; Hydroxylation; Signal.				
FT	SIGNAL	1	19		POTENTIAL.
FT	PROPEP	20	48		

[illegible]

QY 1 MRCLPVPVILLTASGPSVDARLKTDDVPLSLFRDNRNAKSTLQRHODKSVCC 53
 DB 1 MRCLPVPVILLTASGPSVDAPKTKDDVPLAPLHDNRNSTLQTLR-KKVC 52

RESULT 4

CX51_CONTE STANDARD; PRT; 62 AA.
 ID Q9U700;
 AC 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 OS Putative conotoxin TX5.1 precursor.
 OC Conus textile (Cloth-of-gold cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6494;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom duct;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins."
 RL J. Biol. Chem. 274:30664-30671(1999).
 RN [2]
 RP ERRATUM.
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:30630-36030(1999).

CC -!- FUNCTION: Not known. Has only been studied at nucleotidic level.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.

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DR EMBL: AF167164; AAP03684.1; -.
 DR PIR: B59147; B59147.
 DR InterPro: IPR004214; Conotoxin.
 DR Pfam: PF02950; Conotoxin; 1.
 KW Toxin; Signal; Amidation.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 48 BY SIMILARITY.
 FT PRPTIDE 49 60 PUTATIVE CONOTOXIN TX5.1.
 FT DISULFID 50 57 BY SIMILARITY.
 FT DISULFID 51 58 BY SIMILARITY.
 FT MOD_RES 60 60 AMIDATION (G-61 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 SQ SEQUENCE 62 AA; 6857 MW; CE29803DEB0DA421 CRC64;

Query Match 51.2%; Score 169.5; DB 1; Length 62;
 Best Local Similarity 63.8%; Pred. No. 1.4e-14;
 Matches 37; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

QY 1 MRCLPVPVILLTASGPSVDARLKTDDVPLSLFRDNRNAKSTLQRHODKSVCCGYKLC 58
 DB 1 MRCLPVPVILLTASGPSVDAPKTKDDVPLAPLHDNRNSTLQTLR-HLNQRCCTFFWC 57

RESULT 5

CXET_CONTE STANDARD; PRT; 67 AA.
 ID CXET_CONTE

AC DT
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Epsilon-conotoxin TxIX precursor (Conotoxin tx5a).
 OS Conus textile (Cloth-of-gold cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6494;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 51-63, AND MASS SPECTROMETRY.
 RC TISSUE=Venom, and Venom duct;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom duct;
 RX MEDLINE=21105969; PubMed=11158371;
 RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 RL Mol. Biol. Evol. 18:120-131(2001).
 RN [4]
 RP SEQUENCE OF 51-63, CARBOHYDRATE-LINKAGE SITE THR-10, AND STRUCTURE BY
 NMR.
 RC TISSUE=Venom;
 RX MEDLINE=99254114; PubMed=10318957;
 RA Rigby A.C., Lucas-Meunier E., Kalume D.E., Czerwies E., Hambe B.,
 RA Dahlqvist I., Fossier P., Baux G., Roepstorff P., Baleja J.D.,
 RA Furie B.C., Furie B., Stenflo J.P.;
 RT "A conotoxin from Conus textile with unusual posttranslational
 RT modifications reduces presynaptic Ca2+ influx."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5758-5763(1999).
 RN [5]
 RP SEQUENCE OF 51-63, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20146306; PubMed=10679974;
 RA Kalume D.E., Stenflo J.P., Czerwies E., Hambe B., Furie B.C.,
 RA Furie B., Roepstorff P.;
 RT "Structure determination of two conotoxins from Conus textile by a
 RT combination of matrix-assisted laser desorption/ionization
 RT time-of-flight and electrospray ionization mass spectrometry and
 RT biochemical methods."
 RL J. Mass Spectrom. 35:145-156(2000).
 CC -!- FUNCTION: Acts at presynaptic membranes, blocking the calcium
 CC channels. Causes hyperactivity upon intracranial injection into
 CC mice. Causes dorsal fins drooping in fish.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- PTM: O-glycan consists of the disaccharide Gal-GalNAc.
 CC -!- MASS SPECTROMETRY: MW=1929.4; METHOD=Electrospray.
 CC -!- MASS SPECTROMETRY: MW=1929.4; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily. Epsilon-type
 CC family.

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EMBL; AF1671167; AAF03687.1; -;
EMBL; AF214958; AAG0386.1; -;
PIR; E59147; E59147.
PIB; LWCT; 08-JUN-99.
DR InterPro; IPR004214; Conotoxin.
PFam; PF02950; Conotoxin; 1.
KW Toxin; Neurotoxin; Presynaptic neurotoxin; Ionic channel inhibitor;
KW Calcium channel inhibitor; Vitamin K; Signal;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Bromination;
KW 3D-structure. 1
FT SIGNAL 1 19 POTENTIAL.
PROPEP 20 50
FT PEPTIDE 51 63 EPSILON-CONOTOXIN TXIX.
FT PROPEP 64 67
FT DISULFID 52 58
FT DISULFID 53 59
FT MOD RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD RES 57 57 BROMINATION.
FT MOD RES 63 63 HYDROXYLATION.
FT CARBOHYD 60 60 O-LINKED (GALNAAC...).
SEQUENCE 67 AA; 7587 MW; 7270505504D6BB3D CRC64;

Query Match 50.5%; Score 167; DB 1; Length 67;
Best Local Similarity 62.3%; Pred.No.3.2e-14;
Matches 33; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 MRCLPVFVILLILLTASGPSVDARKLTKDDVPLSSFRDNASTLQRHODKSVCC 53
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : |
DB 1 MRCPVFVILLILLIASAPCFDARTKDDVPLSSLRDLNKLRTIRLNRECC 53

RESULT 6
CX51_CONGL STANDARD; PRT; 63 AA.
AC Q9U6Z9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Putative conotoxin Gn5.1 precursor.
OS Conus gloriamaris (Glory of the sea).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbecoconcha; Hypsgastropoda;
OC Negastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37336;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom duct;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RA "The T-superfamily of conotoxins.";
RT J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RL J. Biol. Chem. 274:36030-36030(1999).
CC !- FUNCTION: Not known. Has only been studied at nucleotidic level.
CC !- SUBCELLULAR LOCATION: Secreted.
CC !- TISSUE SPECIFICITY: Expressed by the venom duct.
CC !- SIMILARITY: Belongs to the conotoxin T-superfamily.

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CC
DR EMBL; AF167165; AAF03685.1; -.
DR PIR; C59147; C59147.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
DR KW Toxin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 50 BY SIMILARITY.
FT PEPTIDE 51 63 PUTATIVE CONOTOXIN GM5.1.
FT DISULFID 52 59 POTENTIAL.
FT DISULFID 53 60 POTENTIAL.
FT QO SEQUENCE 63 AA; 7398 MW; 00B24439B5DDE272 CRC64;
Query Match 44.7%; Score 148; DB 1; Length 63;
Best Local Similarity 58.5%; Pred. No. 7.4e-12;
Matches 31; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
QY 1 MRCLPVFVILLLLTASGPSVDAELKTKDDVPLSSFRDNAKSTLQRHQDKSVCC 53
DB 1 MRYLPVFLVILLLLIASPSDTVQLTKDDMPFLASPHGNGRRILMLSNKRLCC 53
RESULT 7
CX51 CONIM STANDARD; PRT; 62 AA.
ID AC Q9UGZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Putative conotoxin IM5.1 precursor.
DE Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_taxID=35631;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom duct;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RA "The T-superfamily of conotoxins.";
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RL J. Biol. Chem. 274:36030-36030(1999).
CC -!- FUNCTION: Not known. Has only been studied at nucleotidic level.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
CC
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CC
CC EMBL; AF167169; AAF03689.1; -.
DR PIR; G59147; G59147.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
DR KW Toxin; Signal; Amidation.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 48 BY SIMILARITY.
FT PEPTIDE 49 60 PUTATIVE CONOTOXIN IM5.1.
FT DISULFID 50 57 BY SIMILARITY.
FT DISULFID 51 58 BY SIMILARITY.

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FT  MOD_RES      60      60      AMIDATION (G-61 PROVIDE AMIDE GROUP)
FT  SEQUENCE     62 AA; 7030 MW; 9570E7C02275796D CRC64;
SQ
Query Match      39.1%; Score 129.5; DB 1; Length 62;
Best Local Similarity 50.8%; Pred. No. 1.5e-09;
Matches 32; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

QY  1 MRCLPVFVILLITAGSPVDRLKTKDDVPLSSFRDNASTLQRHODKSVCCGYKL-CF 59
Db  1 MYCLPVFIILLIISAPSTPPQPRNKDRVHLLSLDNHKKQILQR--DNWSCCGKNPGCC 58

QY  60 PCG 62
Db  59 PWG 61

RESULT 8
CXLI_CONMR      STANDARD; PRT; 11 AA.
AC  P58607;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DE  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Lambda-conotoxin CmrvIA.
OS  Conus marmoreus (Marble cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=42752;
RN  [1]
RP  SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC  TISSUE=Venom;
RX  MEDLINE=20564325; PubMed=10988292;
RA  Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA  Seow K.T., Bay B.-H.;
RT  "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT  pattern and protein folding. Isolation and characterization from the
RT  venom of Conus marmoreus."
RL  J. Biol. Chem. 275:39516-39522(2000).
CC  -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
KW  Neurotoxin; Toxin; Hydroxylation.
FT  DISULFID 2 11
FT  MOD_RES 10 10 HYDROXYLATION.
FT  DISULFID 3 8
FT  MOD_RES 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;
SQ  SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match      20.5%; Score 68; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  51 VCCGYKLCFFPC 61
Db  1 VCCGYKLCFFPC 11

RESULT 9
CXLI_CONMR      STANDARD; PRT; 13 AA.
AC  P58610;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DE  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Lambda/chi-conotoxin MrIB (Chi-MrIB).
OS  Conus marmoreus (Marble cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=42752;
RN  [1]
RP  SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
RC  TISSUE=Venom;
RX  MEDLINE=21419681; PubMed=11528421;
RA  Sharpe I.A., Gehrman J., Loughnan M.L., Thomas L., Adams D.A.,
RA  Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
RA  Lewis R.J.;
RT  "Two new classes of conopeptides inhibit the alpha-adrenoceptor and
RT  noradrenaline transporter."
RL  Nat. Neurosci. 4:902-907(2001).
CC  -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -!- PTM: Exists in two forms, due to cis-trans isomerization at His-
CC  11-Hyp-12.
CC  -!- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
CC  -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
DR  PDB; 1BO; 03-APR-02.
KW  Neurotoxin; Toxin; Hydroxylation; 3D-structure.
FT  DISULFID 4 13
FT  DISULFID 5 10
FT  MOD_RES 12 12 HYDROXYLATION.
FT  MOD_RES 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;
SQ  SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;

Query Match      20.5%; Score 68; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  51 VCCGYKLCFFPC 61
Db  3 VCCGYKLCFFPC 13

RESULT 10
HEMA_VACCT      STANDARD; PRT; 315 AA.
AC  P16561;
DT  01-AUG-1990 (Rel. 15, Created)
DT  01-AUG-1990 (Rel. 15, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Hemagglutinin precursor.
GN  HA OR A56R.
OS  Vaccinia virus (strain Tian Tan).
OC  Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC  Orthopoxvirus.
OX  NCBI_TaxID=10253;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89328331; PubMed=27543392;
RA  Dongyan J., Zhiliang L., Qi J., Hao Y., Yunde H.;
RT  "Vaccinia virus hemagglutinin. A novel member of the immunoglobulin
RT  superfamily."
RL  J. Exp. Med. 170:571-576(1989).
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- PTM: Glycosylated; contains phosphate and sulfate-substituted
CC  glycans. O-glycosylation is required for hemagglutination and
CC  hemadsorption activities of infected cell membranes.
CC  -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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EMBL; X15709; CAA33740.1; -.
DR  PIR; JLO108; HNVZVT.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003599; Ig.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00409; IG; 1.

```


DR	EMBL; M80360; AAA40052.1; --
DR	EMBL; L10319; AAB60711.1; --
DR	EMBL; L10295; AAB60711.1; JOINED.
DR	EMBL; L10296; AAB60711.1; JOINED.
DR	EMBL; L10297; AAB60711.1; JOINED.
DR	EMBL; L10298; AAB60711.1; JOINED.
DR	EMBL; L10299; AAB60711.1; JOINED.
DR	EMBL; L10300; AAB60711.1; JOINED.
DR	EMBL; L10301; AAB60711.1; JOINED.
DR	EMBL; L10304; AAB60711.1; JOINED.
DR	EMBL; L10305; AAB60711.1; JOINED.
DR	EMBL; L10306; AAB60711.1; JOINED.
DR	EMBL; L10307; AAB60711.1; JOINED.
DR	EMBL; L10308; AAB60711.1; JOINED.
DR	EMBL; L10309; AAB60711.1; JOINED.
DR	EMBL; L10310; AAB60711.1; JOINED.
DR	EMBL; L10311; AAB60711.1; JOINED.
DR	EMBL; L10312; AAB60711.1; JOINED.
DR	EMBL; L10313; AAB60711.1; JOINED.
DR	EMBL; L10315; AAB60711.1; JOINED.
DR	EMBL; L10316; AAB60711.1; JOINED.
DR	EMBL; L10317; AAB60711.1; JOINED.
DR	EMBL; L10318; AAB60711.1; JOINED.
DR	EMBL; M24919; AAA40051.1; ALT_SEQ.
DR	PIR; A32495; A32495.
DR	MGD; MGI:109519; MSH3.
DR	InterPro; IPR000432; MutS_C.
DR	InterPro; IPR007860; MutS_II.
DR	InterPro; IPR007696; MutS_III.
DR	InterPro; IPR007695; MutS_N.
DR	Pfam; PF01624; MutS_I; 1.
DR	Pfam; PF05188; MutS_II; 1.
DR	Pfam; PF05192; MutS_III; 1.
DR	Pfam; PF00488; MutS_V; 1.
DR	ProDom; PD001263; MutS_C; 1.
DR	SMART; SM00534; MUTSac; 1.
DR	SMART; SM00533; MUTSad; 1.
DR	PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
KW	DNA repair; ATP-binding; DNA-binding.
FT	NP BIND 850 857 ATP (POTENTIAL).
FT	CONFLICT 505 506 MV -> IL (IN REF. 2).
FT	CONFLICT 864 864 T -> A (IN REF. 2).
SQ	SEQUENCE 1091 AA; 123074 MW; 822BF422436FD513 CRC64;
 Query Match 17.5%; Score 58; DB 1; Length 1091; Best Local Similarity 32.1%; Pred. No. 34; Matches 18; Conservative 5; Mismatches 17; Indels 16; Gaps	
QY	17 GPSVDARLTKTDVPLSSFRDNAAKSTL-----QRHQDKSYC--CGYKLGF 59 : : 164 GPCPEVFQTSCKP---FNKRSKSVYTPLEQLYLDMKQHDKAVLCVEGKYKYP 216
Db	
 RESULT 13	
ID	YANC SCHPO
ID	_YANC SCHPO STANDARD; PRT; 1131 AA.
AC	Q10077;
DT	01-FEB-1996 (Rel. 33, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DE	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Hypothetical protein C3HL12c in chromosome 1.
GN	SPAC3HL12C.
OS	Schizosaccharomyces pombe (Fission yeast).
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;
OC	Schizosaccharomycetes.
OX	NCBI_TaxID=4896;
RN	[1]_TaxID=4896;
RP	SEQUENCE FROM N.A.
RC	STRAIN=972;
RX	MEDLINE=21848401; PubMed=11859360;
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R. Stewart A.,

RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=89178677; PubMed=2926820;
RA Dibb N.J., Maruyama I.N., Krause M., Karn J.;
RT "Sequence analysis of the complete Caenorhabditis elegans myosin
heavy chain gene family.";
RL J. Mol. Biol. 205:603-613(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Harris B.R.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Muscle contraction.
CC -!- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2
heavy chain subunits (MHC), 2 alkali light chain subunits (MLC)
and 2 regulatory light chain subunits (MLC-2).
CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC -!- DOMAIN: The rodlike tail sequence is highly repetitive, showing
cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
characteristic for alpha-helical coiled coils.
CC -!- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light
meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be
split further into 2 globular subfragments (S1) and 1 rod-shaped
subfragment (S2).
CC -!- MISCELLANEOUS: There are four different myosin heavy chains in
C.elegans.
CC -!- MISCELLANEOUS: MHC A and MHC B are found exclusively in the body
wall muscle. They co-assemble into body wall thick filament.
CC -!- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -!- SIMILARITY: Contains 1 IQ domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X08067; CAA30856.1; -
CC EMBL; Z78199; CAB01576.1; -
CC PIR; T23622; S02771.
CC HSP; P08799; IAMD.
CC WormPep; K12F2.1; CE12204.
CC InterPro; IPR000048; IQ region.
CC InterPro; IPR001609; myosin head.
CC InterPro; IPR004609; Myosin_N.
CC InterPro; IPR002928; Myosin_Tail.
CC Pfam; PF00612; IQ; 1.
CC Pfam; PF00063; myosin head; 1.
CC Pfam; PF02736; Myosin_N; 1.
CC Pfam; PF01576; Myosin_Tail; 1.
CC PRINTS; PR00193; MYOSINHEAVY.
CC PRODOM; PD000355; myosin_head; 1.
CC SMART; SM00015; IQ; 1.
CC SMART; SM00242; MYSC; 1.
CC PROSITE; PS50096; IQ; 1.
CC Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
ATP-binding; Methylation; Multigene family.
FT DOMAIN 1 793 MYOSIN HEAD-LIKE.
FT DOMAIN 794 823 IQ.
FT DOMAIN 857 1969 COILED COIL (POTENTIAL).
FT NP BIND 179 186 ATP.
FT DOMAIN 667 689 ACTIN-BINDING.
FT DOMAIN 770 784 ACTIN-BINDING.
FT MOD RES 130 130 METHYLATION (TRI-) (POTENTIAL).
FT CONFLICT 116 116 Y -> YVRKLIKPKKINTIQLNLFQ (IN REF.
2).
SQ SEQUENCE 1969 AA; 225509 MW; 64577BBAF7EAD80A CRC64;
Query Match 17.5%; Score 58; DB 1; Length 1969;
Best Local Similarity 27.1%; Pred No. 63;
Matches 13; Conservative 12; Mismatches 21; Indels 2; Gaps 1;

KY 2 RCLPVEVILLTASGFSVDARLTKDDVPLSSFRDNKAKSTLQRHQDK 49
DB 284 RCYHIF--YQIMSGNDFSLRGKLSNDITYHFCQAELTIEGWDDK 329
RESULT 15
PUR2_YEAST STANDARD; PRT; 802 AA.
ID PUR2_YEAST
AC P07244;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bifunctional purine biosynthetic protein ADE5,7 [Includes:
Phosphoribosylamine-glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide
phosphoribosyltransferase) (Phosphoribosylglycinamide synthetase);
Ribonucleotide synthetase) (Phosphoribosylcyclo-ligase (EC 6.3.3.1) (AIRS)
(Phosphoribosyl-aminimidazole synthetase) (AIR synthase)].
DE ADE5,7 OR YGL234W.
GN Saccharomyces cerevisiae (Baker's yeast).
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87061006; PubMed=3097325;
RA Henikoff S.;
RT "The Saccharomyces cerevisiae ADE5,7 protein is homologous to
overlapping Drosophila melanogaster Gart polypeptides.";
RL J. Mol. Biol. 190:519-528(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Partmann B., Kramer B., Kramer W.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE OF 1-13.
RC STRAIN=S288C;
RX MEDLINE=96093904; PubMed=7483834;
RA Boucherie H., Dujardin G., Kermorgant M., Monribot C., Slonimski P.P.,
Perrot M.;
RA "Two-dimensional protein map of Saccharomyces cerevisiae:
RT construction of a gene-protein index.";
RL Yeast 11:601-613(1995).
CC -!- CATALYTIC ACTIVITY: ATP + 5-phospho-D-ribosylamine + glycine = ADP
+ phosphate + N(1)-(5-phospho-D-ribosyl)glycinamide.
CC -!- CATALYTIC ACTIVITY: ATP + 2-(formamido)-N(1)-(5-phospho-D-
ribosyl)acetamide = ADP + phosphate + 5-amino-1-(5-phospho-D-
ribosyl)imidazole.
CC -!- PATHWAY: De novo purine biosynthesis; second step.
CC -!- PATHWAY: De novo purine biosynthesis; fifth step.
CC -!- SIMILARITY: In the N-terminal section; belongs to the GARS family.
CC -!- SIMILARITY: In the C-terminal section; belongs to the AIR synthase
family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X04337; CAA27867.1; -
CC EMBL; Z72756; CAA96952.1; -
CC PIR; A26343; A26343.
CC HSP; P08178; 1CU1.
CC GERMOnline; 141283; -
CC SGD; S0003203; ADE5,7.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC InterPro; IPR000728; AIR synth.
CC InterPro; IPR000115; Gars.
CC InterPro; IPR004733; PurM_Cligase.
CC Pfam; PF00586; AIRS; 1.

DR Pfam; PF02769; AIRS_C; 1.
DR Pfam; PF01071; GARS; 1.
DR Pfam; PF02842; GARS_B; 1.
DR Pfam; PF02843; GARS_C; 1.
DR Pfam; PF02844; GARS_N; 1.
DR TIGRFAMs; TIGR00877; purD; 1.
DR TIGRFAMs; TIGR00878; purM; 1.
DR PROSITE; PS00184; GARS; 1.
KW Multifunctional enzyme; Purine biosynthesis; Ligase.
FT DOMAIN 1 450
FT DOMAIN 451 802
SQ SEQUENCE 802 AA; 86068 MW; 1583C6F3E64085D2 CRC64;

Query Match 17.4%; Score 57.5; DB 1; Length 802;
Best Local Similarity 30.2%; Pred. No. 28;
Matches 19; Conservative 8; Mismatches 11; Indels 25; Gaps 3;

QY 4 LPVFVILLLLTASGPSVDA-----RLTKDDVPLSSF-----RDNAKSTLQRHQ 47
Db 94 IPVF-----GPSVKAAQLKASKAFSKRFMSKHNIPTASYDVFTNPEEISFLQAH 144

QY 48 DKS 50
Db 145 DKA 147

Search completed: August 10, 2004, 16:03:04
Job time : 13.4054 secs

blank sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 15:59:20 ; Search time 56.1351 Seconds
(without alignments)
348.483 Million cell updates/sec

Title: US-10-072-602B-352

Perfect score: 331

Sequence: 1 MRCLPVFVILLITAGSPSV.....LQRHQDKSVCCGYKLCFPCG 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_ivirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276	83.4	64	5 Q9BPE9	Q9bpe9 conus penna
2	196	59.2	64	5 Q9BPF1	Q9bpf1 conus penna
3	192	58.0	63	5 Q9BPG9	Q9bpg9 conus texti
4	186	56.2	61	5 Q9BH21	Q9bh21 conus texti
5	186	56.2	62	5 Q9BH86	Q9bh86 conus penna
6	183	55.3	61	5 Q9BPF2	Q9bpf2 conus penna
7	183	55.3	63	5 Q9BPE7	Q9bpe7 conus ventr
8	182	55.0	62	5 Q9BPG0	Q9bpg0 conus penna
9	181	54.7	64	5 Q9BPF3	Q9bpf3 conus penna
10	180	54.4	62	5 Q9BPG8	Q9bpg8 conus penna
11	177.5	53.6	59	5 Q9BPF6	Q9bpf6 conus textu
12	177	53.5	64	5 Q9BPF7	Q9bpf7 conus ventr
13	174.5	52.7	63	5 Q9BPF8	Q9bpf8 conus penna
14	173	52.3	58	5 Q9BPH1	Q9bph1 conus texti
15	170.5	51.5	63	5 Q9BPF4	Q9bpf4 conus penna
16	169.5	51.2	61	5 Q9BPF9	Q9bpf9 conus texti

17	168.5	50.9	69	5	Q9BPF0	Q9bpf0 conus penna
18	165.5	50.0	65	5	Q9BPF5	Q9bpf5 conus tessu
19	162	48.9	67	5	Q9BPG6	Q9bpg6 conus texti
20	161	48.6	64	5	Q9BH75	Q9bh75 conus tessu
21	160.5	48.5	69	5	Q9BPE8	Q9bpe8 conus penna
22	160	48.3	60	5	Q9BH99	Q9bh99 conus penna
23	158.5	47.9	63	5	Q9BFG7	Q9bfg7 conus texti
24	158.5	47.9	63	5	Q9BPH0	Q9bph0 conus texti
25	155.5	47.0	60	5	Q9BPH2	Q9bph2 conus penna
26	154	46.5	60	5	Q9BPG5	Q9bpg5 conus ventr
27	154	46.5	61	5	Q9BPG3	Q9bpg3 conus ventr
28	153	46.2	64	5	Q9BEE4	Q9bee4 conus tessu
29	150	45.3	64	5	Q9BPE6	Q9bpe6 conus tessu
30	145	43.8	65	5	Q9BPE5	Q9bpe5 conus tessu
31	139	42.0	61	5	Q9BPG2	Q9bpg2 conus ventr
32	130	39.3	61	5	Q9BPG1	Q9bpg1 conus ventr
33	99.5	30.1	45	5	Q9BPG4	Q9bpg4 conus ventr
34	80	24.2	74	5	Q9BPD9	Q9bpd9 conus tessu
35	74	22.4	66	5	Q9BPE2	Q9bpe2 conus penna
36	73	22.1	77	5	Q9BPS1	Q9bps1 conus arena
37	72.5	21.9	67	5	Q9BH81	Q9bh81 conus arena
38	71	21.5	77	5	Q9BHA6	Q9bha6 conus arena
39	69	20.8	75	5	Q9BPE1	Q9bpe1 conus ventr
40	69	20.8	75	5	Q9BPE0	Q9bpe0 conus ventr
41	68.5	20.7	68	5	Q9BH79	Q9bh79 conus arena
42	67	20.2	65	5	Q9BPD5	Q9bpd5 conus ventr
43	67	20.2	65	5	Q9BPD6	Q9bpd6 conus ventr
44	67	20.2	76	5	Q9BPD2	Q9bpd2 conus arena
45	66.5	20.1	123	10	Q9S703	Q9s703 zea mays (m

ALIGNMENTS

RESULT 1

Q9BPE9 PRELIMINARY; PRT; 64 AA.
AC Q9BPE9
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Conotoxin scaffold IX.
OS Conus pennaceus (feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorboconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214980; AAG60408.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
SQ SEQUENCE 64 AA; 6928 MW; 0AB87620FCCC1410 CRC64;

Query Match

Best Local Similarity 83.4%; Score 276; DB 5; Length 64;

Matches 54; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 1 MRCLPVFVILLITAGSPSVDAAR--LTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLC 58
Db 1 MRCLPVFVILLITAGSPSVDAKVLHNTKGGPLSSFRDNAKSTLQRHQDKSVCCGYKLC 60

Qy 59 FPCG 62

Db 61 VPCG 64

Db 1 MRCLPVFVILLIILIASPSVDAQPKTKDDIPQASFLDNKRYLQVLESKRNCRRQIC-- 58

RESULT 2
Q9BPF1 PRELIMINARY; PRT; 64 AA.
ID Q9BPF1
AC Q9BPF1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conotoxin scaffold IX.
OS Conus pennaceus (feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214978; AAG60406.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
SQ SEQUENCE 64 AA; 7374 MW; F7C8CD0192FC5C8E CRC64;

Query Match 59.2%; Score 196; DB 5; Length 64;
Best Local Similarity 68.3%; Pred. No. 3.6e-18;
Matches 41; Conservative 3; Mismatches 14; Indels 2; Gaps 1;
QY 1 MRCLPVFVILLIILIASPSVDAQPKTKDDIPQASFLDNKRYLQVLESKRNCRRQIC--GKLC 58
Db 1 MRCLPVFVILLIILIASPSVDAQPKTKDDIPQASFLDNKRYLQVLESKRNCRRQIC-- 60

RESULT 3
Q9BPG9 PRELIMINARY; PRT; 63 AA.
ID Q9BPG9
AC Q9BPG9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conotoxin scaffold IX.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214959; AAG60387.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
SQ SEQUENCE 63 AA; 7091 MW; 8AADCFCB2F12EF0A CRC64;

Query Match 58.0%; Score 192; DB 5; Length 63;
Best Local Similarity 64.5%; Pred. No. 1.2e-17;
Matches 40; Conservative 6; Mismatches 14; Indels 2; Gaps 1;
QY 1 MRCLPVFVILLIILIASPSVDAQPKTKDDIPQASFLDNKRYLQVLESKRNCRRQIC-- 60

Db 1 MRCLPVFVILLIILIASPSVDAQPKTKDDIPQASFLDNKRYLQVLESKRNCRRQIC-- 58
QY 61 CG 62
Db 59 CG 60
RESULT 4
Q9BH21 PRELIMINARY; PRT; 61 AA.
ID Q9BH21
AC Q9BH21
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conotoxin scaffold IX precursor.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF215096; AAG60517.1; -.
DR EMBL; AF214963; AAG60391.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
SQ SEQUENCE 61 AA; 6697 MW; FBCAA26F92EB8900 CRC64;

Query Match 56.2%; Score 186; DB 5; Length 61;
Best Local Similarity 71.7%; Pred. No. 7.1e-17;
Matches 38; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
QY 1 MRCLPVFVILLIILIASPSVDAQPKTKDDIPQASFLDNKRYLQVLESKRNCRRQIC-- 53
Db 1 MRCLPVFVILLIILIASPSVDAQPKTKDDIPQASFLDNKRYLQVLESKRNCRRQIC-- 53

RESULT 5
Q9BH86 PRELIMINARY; PRT; 62 AA.
ID Q9BH86
AC Q9BH86
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conotoxin scaffold IX precursor.
OS Conus pennaceus (feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF215098; AAG60519.1; -.
DR EMBL; AF214954; AAG60382.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
SQ SEQUENCE 62 AA; 7127 MW; 45D7118669BD051C CRC64;

RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides." ;
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214976; AAG60404.1; -.

DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	InterPro; IPR004214; Conotoxin.
DR	Pfam; PF02950; Conotoxin; 1.
SQ	SEQUENCE 64 AA; 7146 MW; 5ESA04C6BADD8 CRC64;
 Query Match 54.7%; Score 181; DB 5; Length 64; Best Local Similarity 62.5%; Pred.No.3.4e-16; Matches 40; Conservative 19; Mismatches 19; Indels 2; Gaps 1;	
QY	1 MRCLPVFVILLLLTASGPSVDARLKTDDVPLSSFRDNAKSTLQRHODKSVCC--GKLC 58 : :
Dd	1 MCCLPEVFILLLLTASAPSDALPKTKDDMSLASFDHNAKRTLIILSNKKRYCCVYDISCC 60 :
QY	59 FPGC 62
Dd	61 LSWG 64
 RESULT 10	
Q9BPG8	PRELIMINARY; PRT; 62 AA.
ID	Q9BPG8 PRELIMINARY; PRT; 62 AA.
AC	Q9BPG8; AC
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Conotoxin scaffold IX.
OS	Conus pennacus (Feathered cone).
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC	Neogastropoda; Conoidea; Conidae; Conus.
OX	NCBI_TaxID=37335;
RN	[1]
RP	SEQUENCE FROM N.A.
FX	MEDLINE=21105969; PubMed=11159371;
RA	Corticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA	Fainzilber M.;
RT	"Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL	Mol. Biol. Evol. 18:120-131(2001).
DR	EMBL; AF214960; AAG60388.1; .
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	InterPro; IPR004214; Conotoxin.
DR	Pfam; PF02950; Conotoxin; 1.
SQ	SEQUENCE 62 AA; 6969 MW; ODA718B08DFA9ED1 CRC64;
 Query Match 54.4%; Score 180; DB 5; Length 62; Best Local Similarity 59.7%; Pred.No.4.5e-16; Matches 37; Conservative 20; Indels 0; Gaps 0	
QY	1 MRCLPVFVILLLLTASGPSVDARLKTDDVPLSSFRDNAKSTLQRHODKSVCCGYKLCP 60 :
Dd	1 MRCLPEVFILLLLTASAPSFDLPKTEDNVPLSSFDHNLKRTRRIHLNIRECCSGWCCP 60 :
QY	61 CG 62
Dd	61 AG 62
 RESULT 11	
Q9BPF6	PRELIMINARY; PRT; 59 AA.
ID	Q9BPF6 PRELIMINARY; PRT; 59 AA.
AC	Q9BPF6; AC
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Conotoxin scaffold IX.
OS	Conus tessulatus.
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC	Neogastropoda; Conoidea; Conidae; Conus.

```

ID Q9BPF8 PRELIMINARY; PRT; 63 AA.
AC Q9BPF8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Conotoxin scaffold IX.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214971; AAG60399.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
SQ SEQUENCE 63 AA; 6878 MW; 27DD9A64D056B548 CRC64;

Query Match 52.7%; Score 174.5; DB 5; Length 63;
Best Local Similarity 60.3%; Pred. No. 2.4e-15;
Matches 38; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 1 MRCLPVFVILLITASGPSVDARLKTDDVPLSSFRDNAKSTLQRHDKSVCC-GYKLCF 59
Db 1 MRCLSVFVILLITASGPSVDARLKTDDVPLSSFRDNAKSTLQRHDKSVCC-GYKLCF 59
QY 60 PCG 62
Db 61 PWG 63

RESULT 14
Q9BPH1 PRELIMINARY; PRT; 58 AA.
AC Q9BPH1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Conotoxin scaffold IX.
OS Conus textile (Cloth-of-gold cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6494;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214956; AAG60384.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF02950; Conotoxin; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 58 AA; 6563 MW; D8B7537B6B9516BBA CRC64;

Query Match 52.3%; Score 173; DB 5; Length 58;

```

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Best Local Similarity 65.0%; Pred. No. 3.5e-15;
Matches 39; Conservative 3; Mismatches 12; Indels 6; Gaps 2;

QY 1 MRCLPVFVILLITASGPSVDARLKTDDVPLSSFRDNAKSTLQRHDKSVCCGYKLC 58
Db 1 MRCLPVFVILLITASGPSVDARLKTDDVPLSSFRDNAKSTLQRHDKSVCCGYKLC 58

RESULT 15
Q9BPF4 PRELIMINARY; PRT; 63 AA.
AC Q9BPF4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Conotoxin scaffold IX.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL; AF214975; AAG60403.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
SQ SEQUENCE 63 AA; 6993 MW; 77ED864BFD7FAE50 CRC64;

Query Match 51.5%; Score 170.5; DB 5; Length 63;
Best Local Similarity 55.6%; Pred. No. 8.2e-15;
Matches 35; Conservative 8; Mismatches 19; Indels 1; Gaps 1;

QY 1 MRCLPVFVILLITASGPSVDARLKTDDVPLSSFRDNAKSTLQRHDKSVCC-GYKLCF 59
Db 1 MRCLPVFVILLITASGPSVDARLKTDDVPLSSFRDNAKSTLQRHDKSVCC-GYKLCF 59
QY 60 PCG 62
Db 61 PWG 63

Search completed: August 10, 2004, 16:04:22
Job time : 57.1351 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 15:55:40 ; Search time 15,5676 Seconds
(without alignments)
217.797 Million cell updates/sec

Title: US-10-072-602B-534
Perfect score: 79
Sequence: 1 SVCCGYKLCFPC 12

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04.*
- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001s.*
 - 5: Geneseq2002s.*
 - 6: Geneseq2003as.*
 - 7: Geneseq2003bs.*
 - 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	79	100.0	12	5	ABG99749	Abg99749 Conus sp
2	79	100.0	62	5	ABG99600	Abg99600 Conus sp
3	69	87.3	13	5	ABG99744	Abg99744 Conus sp
4	69	87.3	61	5	ABG99585	Abg99585 Conus sp
5	68	86.1	12	3	ABG99585	Abg99585 Conus sp
6	68	86.1	13	3	ABG99585	Abg99585 Conus sp
7	68	86.1	13	3	ABG99585	Abg99585 Conus sp
8	68	86.1	13	3	ABG99585	Abg99585 Conus sp
9	68	86.1	61	3	ABG99585	Abg99585 Conus sp
10	68	86.1	61	3	ABG99585	Abg99585 Conus sp
11	68	86.1	61	5	ABG99585	Abg99585 Conus sp
12	63	79.7	11	5	ABG99748	Abg99748 Conus sp
13	63	79.7	12	5	ABG99743	Abg99743 Conus sp
14	63	79.7	12	5	ABG99742	Abg99742 Conus sp
15	63	79.7	12	5	ABG99741	Abg99741 Conus sp
16	63	79.7	13	5	ABG99753	Abg99753 Conus sp
17	63	79.7	13	5	ABG99740	Abg99740 Conus sp
18	63	79.7	13	5	ABG99750	Abg99750 Conus sp
19	63	79.7	16	5	ABG99602	Abg99602 Conus sp
20	63	79.7	61	5	ABG99400	Abg99400 Conus sp
21	63	79.7	61	5	ABG99598	Abg99598 Conus sp
22	63	79.7	62	5	ABG99591	Abg99591 Conus sp
23	63	79.7	64	5	ABG99470	Abg99470 Conus sp
24	63	79.7	64	5	ABG99587	Abg99587 Conus sp
25	63	79.7	64	5	ABG99587	Abg99587 Conus sp

26	63	79.7	64	5	ABG99608	Conus sp
27	63	79.7	64	5	ABG99593	Conus sp
28	62	78.5	12	3	ABG99601	Amino aci
29	62	78.5	12	5	ABG99601	Conus sp
30	59	74.7	12	5	ABG99747	Conus sp
31	59	74.7	12	5	ABG99738	Conus sp
32	59	74.7	12	5	ABG99751	Conus sp
33	59	74.7	13	5	ABG99746	Conus sp
34	59	74.7	62	5	ABG99517	Conus sp
35	59	74.7	62	5	ABG99604	Conus sp
36	58	73.4	12	5	ABG99752	Conus sp
37	58	73.4	62	5	ABG99606	Conus sp
38	55	69.6	14	5	ABG99754	Conus sp
39	55	69.6	16	5	ABG99610	Conus sp
40	54	68.4	12	3	ABG99610	Conus sp
41	54	68.4	12	3	ABG99610	Conus sp
42	54	68.4	12	5	ABG99592	Conus sp
43	54	68.4	13	3	ABG99588	Conus sp
44	54	68.4	13	5	ABG99588	Conus sp
45	54	68.4	13	5	ABG99471	Conus sp

ALIGNMENTS

RESULT 1
ID ABG99749 standard; peptide; 12 AA.
XX
AC ABG99749;
XX
DT 17-JAN-2003 (first entry)
XX
DE Conus sp conotoxin-associated peptide SEQ ID 534.
XX
KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
XX ligand-gated ion channel modulator; pain-relief.
XX
OS Conus aulicus.
XX
PN WO200264740-A2.
XX
PD 22-AUG-2002.
XX
PF 11-FEB-2002; 2002WO-US003887.
XX
PR 09-FEB-2001; 2001US-0267408P.
XX
PA (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Olivera BW, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
PI Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
XX WPI; 2002-706921/76.
XX
PT New cone snail conotoxin peptides, useful as a pain reliever for
PT alleviating pain in an individual suffering from pain or who is about to
PT be subjected to a pain-causing event, or for treating voltage-gated ion
PT channel disorders.
XX
PS Claim 1; Page 287; 305pp; English.
XX
CC This invention describes novel conotoxin peptides from the cone snail,
CC genus Conus which have analgesic activity and can act as a voltage-gated
CC ion channel modulator or a ligand-gated ion channel modulator. The
CC conotoxin peptide is useful as a pain-relieving agent for alleviating
CC pain in an individual who is either exhibiting pain or is about to be
CC subjected to a pain-causing event. The conotoxin peptide is also useful
CC for treating or preventing disorders associated with voltage-gated ion
CC channel disorders. ligand-gated ion channel disorders or receptor
CC disorders. The radiolabeled conotoxin peptide is also useful for
CC characterising a new site on these receptors or channels, and for

Wed Aug 11 13:19:37 2004

Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVCCGYKLCFPC 12
| | | | | | | | | | | | | |
Db 50 SVCCGYKLCFPC 61

RESULT 3
ABG99744
ID ABG99744 standard; peptide; 13 AA.
XX AC
XX ABG99744;
XX AC
DT 17-JAN-2003 (first entry)
XX

Conus sp conotoxin-associated peptide SEQ ID 529.
Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
KW ligand-gated ion channel modulator; pain-relief.
XX Conus marmoreus.
OS
XX WO200264740-A2.
PN
XX
XX 22-AUG-2002.
PD
XX
XX 11-FEB-2002; 2002WO-US003887.
PF
XX
XX 09-FEB-2001; 2001US-0267408P.
PR
XX
XX (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
PA

Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
PI Grillley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
XX WPI; 2002-706921/76.
XX
XX New cone snail conotoxin peptides, useful as a pain reliever for
PT alleviating pain in an individual suffering from pain or who is about to
PT be subjected to a pain-causing event, or for treating voltage-gated ion
PT channel disorders.
XX
XX Claim 1; Page 287; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail,
genus Conus which have analgesic activity and can act as a voltage-gated
ion channel modulator or a ligand-gated ion channel modulator. The
conotoxin peptide is useful as a pain-relieving agent for alleviating
pain in an individual who is either exhibiting pain or is about to be
subjected to a pain-causing event. The conotoxin peptide is also useful
for treating or preventing disorders associated with voltage-gated ion
channel disorders, ligand-gated ion channel disorders or receptor
disorders. The radiolabeled conotoxin peptide is also useful for
characterising a new site on these receptors or channels, and for
screening and identifying novel small molecules that interact with the
above-mentioned channels or receptors, which are monamine transporters.
ABG99360-ABG99853 represent the conotoxin protein and peptides described
in the disclosure of the invention

Query Match 87.3%; Score 69; DB 5; Length 13;
Best Local Similarity 90.9%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 VCCGYKLCFPC 12
| | | | | | | | | | | | | |
Db 3 VCCGYKLCFPC 13

RESULT 4

screening and identifying novel small molecules that interact with the
above-mentioned channels or receptors, which are monamine transporters.
ABG99360-ABG99853 represent the conotoxin protein and peptides described
in the disclosure of the invention
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 79; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVCCGYKLCFPC 12
| | | | | | | | | | | | | |
Db 1 SVCCGYKLCFPC 12

RESULT 2
ABG99600
ID ABG99600 standard; protein; 62 AA.
XX AC
XX ABG99600;
XX AC
DT 17-JAN-2003 (first entry)
XX

Conus sp conotoxin-associated protein SEQ ID 352.
Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
KW ligand-gated ion channel modulator; pain-relief.
XX Conus aulicus.
OS
XX WO200264740-A2.
PN
XX
XX 22-AUG-2002.
PD
XX
XX 11-FEB-2002; 2002WO-US003887.
PF
XX
XX 09-FEB-2001; 2001US-0267408P.
PR
XX
XX (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
PA

Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
PI Grillley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
XX WPI; 2002-706921/76.
XX N-PSDB; ABX04937.
XX
XX New cone snail conotoxin peptides, useful as a pain reliever for
PT alleviating pain in an individual suffering from pain or who is about to
PT be subjected to a pain-causing event, or for treating voltage-gated ion
PT channel disorders.
XX
XX Claim 1; Page 239; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail,
genus Conus which have analgesic activity and can act as a voltage-gated
ion channel modulator or a ligand-gated ion channel modulator. The
conotoxin peptide is useful as a pain-relieving agent for alleviating
pain in an individual who is either exhibiting pain or is about to be
subjected to a pain-causing event. The conotoxin peptide is also useful
for treating or preventing disorders associated with voltage-gated ion
channel disorders, ligand-gated ion channel disorders or receptor
disorders. The radiolabeled conotoxin peptide is also useful for
characterising a new site on these receptors or channels, and for
screening and identifying novel small molecules that interact with the
above-mentioned channels or receptors, which are monamine transporters.
ABG99360-ABG99853 represent the conotoxin protein and peptides described
in the disclosure of the invention

Query Match 100.0%; Score 79; DB 5; Length 62;
QY
Db
SQ Sequence 62 AA;

ABG99585
 ID ABG99585 standard; protein; 61 AA.
 XX AC ABG99585;
 XX DT 17-JAN-2003 (first entry)
 XX DE Conus sp conotoxin-associated protein SEQ ID 330.
 XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 KW ligand-gated ion channel modulator; pain-relief.
 XX OS Conus marmoreus.
 XX PN WO200264740-A2.
 XX PD 22-AUG-2002.
 XX PF 11-FEB-2002; 2002WO-US003887.
 XX PR 09-FEB-2001; 2001US-0267408P.
 XX PA (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JB, Cruz LJ;
 PI Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX N-PSDB; ABX04930.
 XX DR New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX PS Claim 1; Page 231; 305pp; English.
 XX CC This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterising a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX SQ Sequence 61 AA;
 Query Match 87.3%; Score 69; DB 5; Length 61;
 Best Local Similarity 90.9%; Pred. No. 0.021;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 VCCGYKLCFPC 12
 Db |||||
 51 VCCGYKLCPC 61
 RESULT 5
 AAB08018
 ID AAB08018 standard; peptide; 12 AA.
 XX AC AAB08018;
 XX DT 14-NOV-2000 (first entry)
 XX DE Amino acid sequence of the conotoxin peptide Mar2.
 XX KW Ap-conotoxin; conotoxin; venom; cone snail; analgesic; pain; Mar2.
 XX OS Conus marmoreus.
 XX FH Key Location/Qualifiers
 FT Modified-site 12
 FT /note= "hydroxy-Pro"
 XX WO200044769-A1.
 XX PN 03-AUG-2000.
 XX PD 28-JAN-2000; 2000WO-US001978.
 XX PR 29-JAN-1999; 99US-0118381P.
 PR 28-DEC-1999; 99US-0173343P.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI McIntosh JM, Olivera BM, Cruz LJ;
 PI WPI; 2000-476222/41.
 XX DR Purified ap-conotoxin derived from cone snail venom for use as an
 PT analgesic.
 XX PS Claim 14; Page; 29pp; English.
 XX CC The present sequence represents an ap-conotoxin peptide, designated Mar2.
 CC Conotoxins are naturally available in minute amounts in the venom of cone
 CC snails. The peptides have analgesic activity. The peptides are used to
 CC treat or prevent pain. note: this sequence does not appear in the
 CC specification; it was created using information provided
 XX SQ Sequence 12 AA;
 Query Match 86.1%; Score 68; DB 3; Length 12;
 Best Local Similarity 90.9%; Pred. No. 0.0072;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 VCCGYKLCFPC 12
 Db |||||
 2 VCCGYKLCPC 12
 RESULT 6
 AAY92229
 ID AAY92229 standard; peptide; 13 AA.
 XX AC AAY92229;
 XX DT 10-AUG-2000 (first entry)
 XX DE Chi-conotoxin peptide, chi-Mr7A.
 XX KW chi-conotoxin; chi-Mr7A; cone snail; inhibitor; amine transporter;
 KW neuronal; noradrenaline transporter; urinary tract disorder; analgesic;
 KW antiarrhythmic; cardiant; antidepressant; anxiolytic; anti-inflammatory.
 XX OS Conus marmoreus.
 XX FH Key Location/Qualifiers
 FT Misc-difference 12
 FT /label= 4Hyp
 FT /note= "4-hydroxyproline"
 XX WO200020444-A1.
 XX PD 13-APR-2000.
 XX PF 01-OCT-1999; 99WO-AU000844.
 XX

```

02-OCT-1998; 98AU-00006274.
(UYQU ) UNIV QUEENSLAND.
Lewis RJ, Alewood PF, Sharpe IA;
WPI; 2000-303738/26.

Isolated, synthetic or recombinant chi-conotoxin peptide capable of
inhibiting neuronal amine transporter used for treatment or prophylaxis
of urinary or cardiovascular conditions, mood disorders, or
treatment/control of pain/inflammation.

Claim 3; Page 33; 47pp; English.

This conotoxin, chi-MrIA, is a member of a new class of conotoxins,
designated chi-conotoxin. It was isolated from the venom of the mollusc
hunting cone snail, Conus marmoreus. The peptide is an inhibitor of the
neuronal amine transporters, especially the neuronal noradrenaline
transporter. Inhibitors of noradrenaline re-uptake which have a
negligible anti-cholinergic effect are particularly useful in the
treatment of lower urinary tract disorders. Chi-MrIA (0.1 nM-1 micro M)
inhibited the accumulation of radiolabeled noradrenaline in a
concentration-dependent manner, with a log IC-50 value of -8.17 plus or
minus 0.0275 (n = 4). The concentration of chi-MrIA required to inhibit
the accumulation by 50 percent was found to be approximately 7 nM. This
concentration is approximately one order of magnitude lower than that
needed for desipramine to produce the same effect. The peptides are
useful for the treatment or prophylaxis of urinary or cardiovascular
conditions or diseases (arrhythmia or coronary heart failure) or mood
disorders (depression, anxiety or cravings), or the treatment or control
of pain or inflammation (chronic pain, neuropathic pain or inflammatory
pain)

Sequence 13 AA;

Query Match 86.1%; Score 68; DB 3; Length 13;
Best Local Similarity 90.9%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VCCGYKLCFPC 12
DB 3 VCCGYKLCFPC 13
|||||
|||||

RESULT 7
AA92230
ID AA92230 standard; peptide; 13 AA.
XX
XX AA92230;
AC
DT 10-AUG-2000 (first entry)
XX
XX Chi-conotoxin peptide, chi-MrIB.
KW chi-conotoxin; chi-MrIB; cone snail; inhibitor; amine transporter;
KW neuronal; noradrenaline transporter; urinary tract disorder; analgesic;
KW antiarrhythmic; cardiant; antidepressant; anxiolytic; anti-inflammatory.
XX
XX Conus marmoreus.
XX
XX Key Location/Qualifiers
FH Misc-difference 12 /label= 4HYP
FT /note= "4-hydroxyproline"
XX
XX WO200020444-A1.
XX
XX 13-APR-2000.
XX
XX 01-OCT-1999; 99WO-AU000844.
XX
XX 02-OCT-1998; 98AU-00006274.
XX

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PI McIntosh JM, Olivera BM, Cruz LJ;
DR WPI; 2000-476222/41.
XX Purified ap-conotoxin derived from cone snail venom for use as an
XX analgesic.
XX
XX Claim 13; Page; 29pp; English.
XX
XX The present sequence represents an ap-conotoxin peptide, designated Marl.
XX Conotoxins are naturally available in minute amounts in the venom of cone
XX snails. The peptides have analgesic activity. The peptides are used to
XX treat or prevent pain. note: this sequence does not appear in the
XX specification; it was created using information provided
XX
XX Sequence 13 AA;
SQ
    Query Match      86.1%; Score 68; DB 3; Length 13;
    Best Local Similarity 90.9%; Pred. No. 0.0077;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VCCGYKLCFPC 12
Db 3 VCCGYKLCFPC 13

RESULT 9
AAAY92231
ID AAAY92231 standard; protein; 61 AA.
XX
AC AAAY92231;
XX
DT 10-AUG-2000 (first entry)
XX
DE Chi-conotoxin, chi-MrIA, leader and mature peptide.
XX
KW Chi-conotoxin; chi-MrIA; cone snail; inhibitor; amine transporter;
KW neuronal; noradrenaline transporter; urinary tract; analgesic; cardiac;
KW antiarrhythmic; antidepressant; anxiolytic; anti-inflammatory.
XX
OS Conus marmoreus.
XX
PN WO200020444-A1.
XX
PD 13-APR-2000.
XX
PF 01-OCT-1999; 99WO-AU000844.
XX
PR 02-OCT-1998; 98AU-00006274.
XX
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Lewis RJ, Alewood PF, Sharpe IA;
XX
DR WPI; 2000-303738/26.
DR N-PSDB; AAA09112.
XX
XX Isolated, synthetic or recombinant chi-conotoxin peptide capable of
XX inhibiting neuronal amine transporter used for treatment or prophylaxis
XX of urinary or cardiovascular conditions, mood disorders, or
XX treatment/control of pain/inflammation.
XX
XX Example 7; Page 31; 47pp; English.
XX
XX This sequence is the conotoxin, chi-MrIA, a member of a new class of
XX conotoxins, designated chi-conotoxin. It was isolated from the venom of
XX the mollusc hunting cone snail, Conus marmoreus. The peptide is an
XX inhibitor of the neuronal amine transporters, especially the neuronal
XX noradrenaline transporter. Inhibitors of noradrenaline re-uptake which
XX have a negligible anti-cholinergic effect are particularly useful in the
XX treatment of lower urinary tract disorders. Chi-MrIA (0.1 nM-1 micro M)
XX inhibited the accumulation of radiolabelled noradrenaline in a
XX concentration-dependent manner, with a log IC-50 value of -8.17 plus or

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```

CC minus 0.0275 (n = 4). The concentration of chi-MrIA required to inhibit
CC the accumulation by 50 percent was found to be approximately 7 nM. This
CC concentration is approximately one order of magnitude lower than that
CC needed for desipramine to produce the same effect. The peptides are
CC useful for the treatment or prophylaxis of urinary or cardiovascular
CC conditions or diseases (arrhythmia or coronary heart failure) or mood
CC disorders (depression, anxiety or cravings), or the treatment or control
CC of pain or inflammation (chronic pain, neuropathic pain or inflammatory
CC pain)
XX
XX Sequence 61 AA;
SQ
    Query Match      86.1%; Score 68; DB 3; Length 61;
    Best Local Similarity 90.9%; Pred. No. 0.028;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VCCGYKLCFPC 12
Db 51 VCCGYKLCFPC 61

RESULT 10
AAB08016
ID AAB08016 standard; protein; 61 AA.
XX
AC AAB08016;
XX
DT 14-NOV-2000 (first entry)
XX
DE Amino acid sequence of the conotoxin Marl propeptide.
XX
KW Ap-conotoxin; conotoxin; venom; cone snail; analgesic; pain; Marl.
XX
OS Conus marmoreus.
XX
PN WO200044769-A1.
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US001978.
XX
PR 29-JAN-1999; 99US-0118381P.
XX
PR 28-DEC-1999; 99US-0173343P.
XX
XX (UTAH ) UNIV UTAH RES FOUND.
XX
XX McIntosh JM, Olivera BM, Cruz LJ;
XX
XX WPI; 2000-476222/41.
XX N-PSDB; AAA63513.
XX
XX Purified ap-conotoxin derived from cone snail venom for use as an
XX analgesic.
XX
XX Claim 23; Page 13-14; 29pp; English.
XX
XX The present sequence represents a Marl propeptide. Marl is an ap-
XX conotoxin peptide. Conotoxins are naturally available in minute amounts
XX in the venom of cone snails. The peptides have analgesic activity. The
XX peptides are used to treat or prevent pain
XX
XX Sequence 61 AA;
SQ
    Query Match      86.1%; Score 68; DB 3; Length 61;
    Best Local Similarity 90.9%; Pred. No. 0.028;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VCCGYKLCFPC 12
Db 51 VCCGYKLCFPC 61

RESULT 11

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ABG99595
 ID ABG99595 standard; protein; 61 AA.
 XX AC ABG99595;
 XX DT 17-JAN-2003 (first entry)
 XX DE Conus sp conotoxin-associated protein SEQ ID 345.
 XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 XX KW ligand-gated ion channel modulator; pain-relief.
 XX OS Conus marmoreus.
 XX PN WO200264740-A2.
 XX PD 22-AUG-2002.
 XX PF 11-FEB-2002; 2002WO-US003887.
 XX PR 09-FEB-2001; 2001US-0267408P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 XX PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX PI WPI; 2002-706921/76.
 XX DR N-PSDB; ABX04935.
 XX DT New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX PS Claim 1; Page 236; 305pp; English.
 XX CC This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterising a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX SQ Sequence 61 AA;
 Query Match 86.1%; Score 68; DB 5; Length 61;
 Best Local Similarity 90.9%; Pred. No. 0.028; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 VCCGYKLCFFC 12
 DB 51 VCCGYKLCFFC 61
 RESULT 12
 ABG99748
 ID ABG99748 standard; peptide; 11 AA.
 XX AC ABG99748;
 XX DT 17-JAN-2003 (first entry)
 XX DE Conus sp conotoxin-associated peptide SEQ ID 533.
 XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 XX KW ligand-gated ion channel modulator; pain-relief.
 XX OS Conus bandanus.
 XX PN WO200264740-A2.
 XX PD 22-AUG-2002.
 XX PF 11-FEB-2002; 2002WO-US003887.
 XX PR 09-FEB-2001; 2001US-0267408P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 XX PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX PI WPI; 2002-706921/76.
 XX DR N-PSDB; ABX04935.
 XX DT New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX PS Claim 1; Page 236; 305pp; English.
 XX CC This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterising a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX SQ Sequence 61 AA;
 Query Match 86.1%; Score 68; DB 5; Length 61;
 Best Local Similarity 90.9%; Pred. No. 0.028; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 VCCGYKLCFFC 12
 DB 51 VCCGYKLCFFC 61
 RESULT 12
 ABG99739
 ID ABG99739 standard; peptide; 11 AA.
 XX AC ABG99739;
 XX DT 17-JAN-2003 (first entry)
 XX DE Conus sp conotoxin-associated peptide SEQ ID 524.
 XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 XX KW ligand-gated ion channel modulator; pain-relief.
 XX OS Conus bandanus.
 XX PN WO200264740-A2.
 XX PD 22-AUG-2002.
 XX PF 11-FEB-2002; 2002WO-US003887.
 XX PR 09-FEB-2001; 2001US-0267408P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 XX PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX PI WPI; 2002-706921/76.
 XX DR N-PSDB; ABX04935.
 XX DT New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX PS Claim 1; Page 287; 305pp; English.
 XX CC This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterising a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX SQ Sequence 11 AA;
 Query Match 79.7%; Score 63; DB 5; Length 11;
 Best Local Similarity 90.0%; Pred. No. 0.032; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 CCGYKLCFFC 12
 DB 2 CCGYKLCFFC 11
 RESULT 13
 ABG99739
 ID ABG99739 standard; peptide; 11 AA.
 XX AC ABG99739;
 XX DT 17-JAN-2003 (first entry)
 XX DE Conus sp conotoxin-associated peptide SEQ ID 524.
 XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 XX KW ligand-gated ion channel modulator; pain-relief.
 XX OS Conus bandanus.
 XX PN WO200264740-A2.
 XX PD 22-AUG-2002.

XX PF 11-FEB-2002; 2002WO-US003887.
 XX PR 09-FEB-2001; 2001US-0267408P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 XX PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX WPI; 2002-706921/76.
 XX New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX Claim 1; Page 286; 305pp; English.
 XX This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterizing a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX Sequence 11 AA;
 SQ Query Match 79.7%; Score 63; DB 5; Length 11;
 Best Local Similarity 90.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 CCGYKLCSPC 12
 Db |||||
 2 CCGYKLCSPC 11
 RESULT 14
 ABG99743
 ID ABG99743 standard; peptide; 12 AA.
 XX AC ABG99743;
 XX DT 17-JAN-2003 (first entry)
 XX DE Conus sp conotoxin-associated peptide SEQ ID 528.
 XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 XX KW ligand-gated ion channel modulator; pain-relief.
 XX OS Conus episcopatus.
 XX PN WO200264740-A2.
 XX PD 22-AUG-2002.
 XX PF 11-FEB-2002; 2002WO-US003887.
 XX PR 09-FEB-2001; 2001US-0267408P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;

PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX WPI; 2002-706921/76.
 XX New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.
 XX Claim 1; Page 286; 305pp; English.
 XX This invention describes novel conotoxin peptides from the cone snail,
 CC genus Conus which have analgesic activity and can act as a voltage-gated
 CC ion channel modulator or a ligand-gated ion channel modulator. The
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating
 CC pain in an individual who is either exhibiting pain or is about to be
 CC subjected to a pain-causing event. The conotoxin peptide is also useful
 CC for treating or preventing disorders associated with voltage-gated ion
 CC channel disorders, ligand-gated ion channel disorders or receptor
 CC disorders. The radiolabeled conotoxin peptide is also useful for
 CC characterizing a new site on these receptors or channels, and for
 CC screening and identifying novel small molecules that interact with the
 CC above-mentioned channels or receptors, which are monoamine transporters.
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
 CC in the disclosure of the invention
 XX Sequence 12 AA;
 SQ Query Match 79.7%; Score 63; DB 5; Length 12;
 Best Local Similarity 66.7%; Pred. No. 0.035;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SVCCGYKLCFPC 12
 Db |||||
 1 STCCGYRMCVPC 12
 RESULT 15
 ABG99742
 ID ABG99742 standard; peptide; 12 AA.
 XX AC ABG99742;
 XX DT 17-JAN-2003 (first entry)
 XX DE Conus sp conotoxin-associated peptide SEQ ID 527.
 XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 XX KW ligand-gated ion channel modulator; pain-relief.
 XX OS Conus pennaceus.
 XX PN WO200264740-A2.
 XX PD 22-AUG-2002.
 XX PF 11-FEB-2002; 2002WO-US003887.
 XX PR 09-FEB-2001; 2001US-0267408P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
 XX PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
 XX WPI; 2002-706921/76.
 XX New cone snail conotoxin peptides, useful as a pain reliever for
 PT alleviating pain in an individual suffering from pain or who is about to
 PT be subjected to a pain-causing event, or for treating voltage-gated ion
 PT channel disorders.

PS Claim 1; Page 286; 305pp; English.

XX This invention describes novel conotoxin peptides from the cone snail,
CC genus Conus which have analgesic activity and can act as a voltage-gated
CC ion channel modulator or a ligand-gated ion channel modulator. The
CC conotoxin peptide is useful as a pain-relieving agent for alleviating
CC pain in an individual who is either exhibiting pain or is about to be
CC subjected to a pain-causing event. The conotoxin peptide is also useful
CC for treating or preventing disorders associated with voltage-gated ion
CC channel disorders, ligand-gated ion channel disorders or receptor
CC disorders. The radiolabeled conotoxin peptide is also useful for
CC characterising a new site on these receptors or channels, and for
CC screening and identifying novel small molecules that interact with the
CC above-mentioned channels or receptors, which are monoamine transporters,
CC ABG99360-ABG99853 represent the conotoxin protein and peptides described
CC in the disclosure of the invention

XX

SQ Sequence 12 AA;

Query Match 79.7%; Score 63; DB 5; Length 12;
Best Local Similarity 66.7%; Pred. No. 0.035;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVCCGYKLCFPC 12
| | | | | | | |
Db 1 STCCGFMCIPC 12

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Job time : 15.5676 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:00:55 ; Search time 4.7027 Seconds
(without alignments)
131.735 Million cell updates/sec

Title: US-10-072-602B-534

Perfect score: 79

Sequence: 1 SVCCGYKLCFP 12

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	45	57.0	187	4	US-09-336-536-60
3	45	57.0	213	4	US-09-336-536-58
4	44	55.7	503	4	US-09-914-259-13
5	43.5	55.1	38	1	US-08-137-800-29
6	43.5	55.1	38	1	US-08-477-383-29
7	43.5	55.1	38	1	US-08-480-750-29
8	43.5	55.1	38	1	US-08-480-750-29
9	43.5	55.1	42	1	US-08-477-383-59
10	43.5	55.1	42	1	US-08-487-174-59
11	43.5	55.1	42	1	US-08-480-750-59
12	43.5	55.1	80	1	US-08-137-800-44
13	43.5	55.1	80	1	US-08-477-383-44
14	43.5	55.1	80	1	US-08-487-174-44
15	43.5	55.1	80	1	US-08-480-750-44
16	42.5	53.8	30	1	US-08-137-800-35
17	42.5	53.8	30	1	US-08-477-383-35
18	42.5	53.8	30	1	US-08-487-174-35
19	42.5	53.8	30	1	US-08-480-750-35
20	42.5	53.8	37	1	US-08-137-800-27
21	42.5	53.8	37	1	US-08-477-383-27
22	42.5	53.8	37	1	US-08-487-174-27
23	42.5	53.8	37	1	US-08-480-750-27
24	42.5	53.8	38	1	US-08-137-800-25
25	42.5	53.8	38	1	US-08-477-383-25
26	42.5	53.8	38	1	US-08-487-174-25
27	42.5	53.8	38	1	US-08-480-750-25

28	42.5	53.8	41	1	US-08-477-383-57	Sequence 57, Appl
29	42.5	53.8	41	1	US-08-487-174-57	Sequence 57, Appl
30	42.5	53.8	41	1	US-08-480-750-57	Sequence 57, Appl
31	42.5	53.8	42	1	US-08-477-383-56	Sequence 56, Appl
32	42.5	53.8	42	1	US-08-487-174-56	Sequence 56, Appl
33	42.5	53.8	42	1	US-08-480-750-56	Sequence 56, Appl
34	42.5	53.8	69	1	US-08-137-800-40	Sequence 40, Appl
35	42.5	53.8	69	1	US-08-477-383-40	Sequence 40, Appl
36	42.5	53.8	69	1	US-08-487-174-40	Sequence 40, Appl
37	42.5	53.8	69	1	US-08-480-750-40	Sequence 40, Appl
38	42.5	53.8	79	1	US-08-137-800-42	Sequence 42, Appl
39	42.5	53.8	79	1	US-08-477-383-42	Sequence 42, Appl
40	42.5	53.8	79	1	US-08-487-174-42	Sequence 42, Appl
41	42.5	53.8	79	1	US-08-480-750-42	Sequence 42, Appl
42	42.5	53.8	80	1	US-08-137-800-41	Sequence 41, Appl
43	42.5	53.8	80	1	US-08-477-383-41	Sequence 41, Appl
44	42.5	53.8	80	1	US-08-487-174-41	Sequence 41, Appl
45	42.5	53.8	80	1	US-08-480-750-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-336-536-65
; Sequence 65, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336.536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-336-536-65

Query Match 57.0%; Score 45; DB 4; Length 56;
Best Local Similarity 63.6%; Pred. No. 7.6;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 SVCCGYKLCFP 11
Db 5 SCCCLYKCCP 15

RESULT 2
US-09-336-536-60
; Sequence 60, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336.536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-336-536-60

Query Match 57.0%; Score 45; DB 4; Length 187;

Best Local Similarity 63.6%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SVCCGYKLCFP 11
Db 106 SCCCLYKMCPP 116

RESULT 3

US-09-336-536-58
; Sequence 58, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-336-536-58

Query Match 57.0%; Score 45; DB 4; Length 213;
Best Local Similarity 63.6%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SVCCGYKLCFP 11
Db 132 SCCCLYKMCPP 142

RESULT 4

US-09-914-259-13
; Sequence 13, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-914-259-13

Query Match 55.7%; Score 44; DB 4; Length 503;
Best Local Similarity 55.6%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CGYKLCFPC 12
Db 150 CGHRCMPC 158

RESULT 5

US-08-137-800-29
; Sequence 29, Application US/08137800
; Patent No. 5514774
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.

; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Santos, Ameurfin D.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,800
; FILING DATE: 19-OCT-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-104763
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus stercusmuscarum
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37..38
; OTHER INFORMATION: /note= "Xaa is des-Xaa or
; OTHER INFORMATION: Gly-Arg-Arg-Asn-His"
US-08-137-800-29
Query Match 55.1%; Score 43.5; DB 1; Length 38;
Best Local Similarity 46.7%; Pred. No. 8.7;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;
Qy 1 SVCCGY---KLCFPC 12
Db 10 TTCGYDPGSMCPPC 24
RESULT 6
US-08-477-383-29
; Sequence 29, Application US/08477383
; Patent No. 5589340
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfin D.
; TITLE OF INVENTION: Conotoxin Peptides
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/477,383
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus stercusmuscarum
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 38
; OTHER INFORMATION: /note= "Xaa is des-Xaa or
; OTHER INFORMATION: Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is
; OTHER INFORMATION: preferably amidated."
US-08-477-383-29

Query Match 55.1%; Score 43.5; DB 1; Length 38;
Best Local Similarity 46.7%; Pred. No. 8.7;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 SVCCGY---KLCFPC 12
Db : ||||| : |||||
10 TTCGYDPGSMCPPC 24

RESULT 7
US-08-487-174-29
; Sequence 29, Application US/08487174
; Patent No. 5595972
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,174
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus stercusmuscarum
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 38
; OTHER INFORMATION: /note= "Xaa is des-Xaa or
; OTHER INFORMATION: Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is
; OTHER INFORMATION: preferably amidated."
US-08-487-174-29

Query Match 55.1%; Score 43.5; DB 1; Length 38;
Best Local Similarity 46.7%; Pred. No. 8.7;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 SVCCGY---KLCFPC 12
Db : ||||| : |||||
10 TTCGYDPGSMCPPC 24

RESULT 8
US-08-480-750-29
; Sequence 29, Application US/08480750
; Patent No. 5633347
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,750
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800

```

; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus stercusmuscarum
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 38
; OTHER INFORMATION: /note= "Xaa is des-Xaa or
; OTHER INFORMATION: Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is
; OTHER INFORMATION: preferably amidated."
US-08-480-750-29

```

```

Query Match 55.1%; Score 43.5; DB 1; Length 38;
Best Local Similarity 46.7%; Pred. No. 8.7;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

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QY 1 SVCCGY---KLCFPC 12
: ||||| : |||
Db 10 TTCGYDPGSMCPPC 24

```

```

RESULT 9
US-08-477-383-59
; Sequence 59, Application US/08477383
; Patent No. 5589340
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfin S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,383
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus stercusmuscarum
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 38
; OTHER INFORMATION: /note= "Xaa is des-Xaa or
; OTHER INFORMATION: Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is
; OTHER INFORMATION: preferably amidated."
US-08-480-750-29

```

```

; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus stercusmuscarum
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 38
; OTHER INFORMATION: /note= "Xaa is des-Xaa or
; OTHER INFORMATION: Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is
; OTHER INFORMATION: preferably amidated."
US-08-477-383-59

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Query Match 55.1%; Score 43.5; DB 1; Length 42;
Best Local Similarity 46.7%; Pred. No. 9.4;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

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QY 1 SVCCGY---KLCFPC 12
: ||||| : |||
Db 10 TTCGYDPGSMCPPC 24

```

```

RESULT 10
US-08-487-174-59
; Sequence 59, Application US/08487174
; Patent No. 5595972
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfin S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,174
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus stercusmuscarum
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 38
; OTHER INFORMATION: /note= "Xaa is des-Xaa or
; OTHER INFORMATION: Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is
; OTHER INFORMATION: preferably amidated."
US-08-480-750-29

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;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Conus stercusmuscarum
US-08-487-174-59

Query Match 55.1%; Score 43.5; DB 1; Length 42;
Best Local Similarity 46.7%; Pred. No. 9.4;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 SVCCGY---KLCFPC 12
: ||||| : |||||
Db 10 TTCCGYDPGSMCPCC 24

RESULT 11
US-08-480-750-59
; Sequence 59, Application US/08480750
; Patent No. 5633347
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus stercusmuscarum
US-08-480-750-59

Query Match 55.1%; Score 43.5; DB 1; Length 42;
Best Local Similarity 46.7%; Pred. No. 9.4;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 SVCCGY---KLCFPC 12
: ||||| : |||||
Db 10 TTCCGYDPGSMCPCC 24

RESULT 12
US-08-137-800-44
; Sequence 44, Application US/08137800
; Patent No. 5514774
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfino D.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-104763
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Conus stercusmuscarum
US-08-137-800-44

Query Match 55.1%; Score 43.5; DB 1; Length 80;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 SVCCGY---KLCFPC 12
: ||||| : |||||
Db 48 TTCCGYDPGSMCPCC 62

RESULT 13
US-08-477-383-44
; Sequence 44, Application US/08477383
; Patent No. 5589340
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:

ADDRESSER: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus stercusmuscarum
US-08-477-383-44

Query Match 55.1%; Score 43.5; DB 1; Length 80;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 SVCCGY---KLCFPC 12
: ||||| : |||||
Db 48 TTCCGYDPGSMCPCC 62

RESULT 14

US-08-487-174-44
Sequence 44, Application US/08487174
Patent No. 5595972
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus stercusmuscarum
US-08-487-174-44

Query Match 55.1%; Score 43.5; DB 1; Length 80;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 SVCCGY---KLCFPC 12
: ||||| : |||||
Db 48 TTCCGYDPGSMCPCC 62

RESULT 15

US-08-480-750-44
Sequence 44, Application US/08480750
Patent No. 5633347
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus stercusmuscarum
US-08-480-750-44

Query Match 55.1%; Score 43.5; DB 1; Length 80;
Best Local Similarity 46.7%; Pred.No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SVCCGY---KLCFPC 12
: ||| : |||
Db 48 TTCCGYDPGSMCPPC 62

Search completed: August 10, 2004, 16:05:36
Job time : 4.7027 secs

blank sheet

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:04:26 ; Search time 13.1351 Seconds

(without alignments)
286.575 Million cell updates/sec

Title: US-10-072-602B-534

Perfect score: 79

Sequence: 1 SVCCGYKLCFFC 12

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	12	14	US-10-072-602B-534
2	79	100.0	62	14	US-10-072-602B-352
3	69	87.3	13	14	US-10-072-602B-529
4	69	87.3	61	14	US-10-072-602B-330
5	68	86.1	61	14	US-10-072-602B-345
6	63	79.7	11	14	US-10-072-602B-524
7	63	79.7	11	14	US-10-072-602B-533
8	63	79.7	12	14	US-10-072-602B-527
9	63	79.7	12	14	US-10-072-602B-528
10	63	79.7	13	14	US-10-072-602B-525
11	63	79.7	13	14	US-10-072-602B-526
12	63	79.7	13	14	US-10-072-602B-535
13	63	79.7	13	14	US-10-072-602B-538
14	63	79.7	16	14	US-10-072-602B-355
15	63	79.7	61	14	US-10-072-602B-62

16	63	79.7	61	14	US-10-072-602B-349	Sequence 349, App
17	63	79.7	62	14	US-10-072-602B-339	Sequence 339, App
18	63	79.7	64	14	US-10-072-602B-162	Sequence 162, App
19	63	79.7	64	14	US-10-072-602B-333	Sequence 333, App
20	63	79.7	64	14	US-10-072-602B-342	Sequence 342, App
21	63	79.7	64	14	US-10-072-602B-364	Sequence 364, App
22	62	78.5	12	14	US-10-072-602B-353	Sequence 353, App
23	59	74.7	12	14	US-10-072-602B-523	Sequence 523, App
24	59	74.7	12	14	US-10-072-602B-532	Sequence 532, App
25	59	74.7	12	14	US-10-072-602B-536	Sequence 536, App
26	59	74.7	13	14	US-10-072-602B-531	Sequence 531, App
27	59	74.7	62	14	US-10-072-602B-229	Sequence 229, App
28	59	74.7	62	14	US-10-072-602B-358	Sequence 358, App
29	58	73.4	12	14	US-10-072-602B-537	Sequence 537, App
30	58	73.4	62	14	US-10-072-602B-361	Sequence 361, App
31	55	69.6	14	14	US-10-072-602B-539	Sequence 539, App
32	55	69.6	16	14	US-10-072-602B-367	Sequence 367, App
33	54	68.4	12	14	US-10-072-602B-340	Sequence 340, App
34	54	68.4	13	14	US-10-072-602B-163	Sequence 163, App
35	54	68.4	13	14	US-10-072-602B-334	Sequence 334, App
36	54	68.4	13	14	US-10-072-602B-365	Sequence 365, App
37	52	65.8	12	14	US-10-072-602B-530	Sequence 530, App
38	52	65.8	13	14	US-10-072-602B-331	Sequence 331, App
39	52	65.8	62	14	US-10-072-602B-336	Sequence 336, App
40	52	65.8	438	15	US-10-262-445-34	Sequence 34, App1
41	51	64.6	12	14	US-10-072-602B-347	Sequence 347, App
42	51	64.6	13	14	US-10-072-602B-346	Sequence 346, App
43	50	63.3	81	12	US-10-424-599-161903	Sequence 161903, App
44	50	63.3	478	12	US-10-425-114-56089	Sequence 56089, App
45	49	62.0	12	14	US-10-072-602B-362	Sequence 362, App

ALIGNMENTS

RESULT 1
US-10-072-602B-534
; Sequence 534 Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 534
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Conus aulicus
US-10-072-602B-534

Query Match 100.0%; Score 79; DB 14; Length 12;

Best Local Similarity 100.0%; Pred.No. 0.0003; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 SVCCGYKLCFFC 12

DB 1 SVCCGYKLCFFC 12

RESULT 2
 US-10-072-602B-352
 ; Sequence 352, Application US/10072602B
 ; Publication No. US20030109670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: McIntosh, J, Michael
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Cruz, Lourdes J.
 ; APPLICANT: Grilley, Michelle
 ; APPLICANT: Schoenfeld, Robert M.
 ; APPLICANT: Walker, Craig
 ; APPLICANT: Shetty, Reshma
 ; APPLICANT: Jones, Robert M.
 ; TITLE OF INVENTION: Cone Snail Peptides
 ; FILE REFERENCE: 2314-249
 ; CURRENT APPLICATION NUMBER: US/10/072,602B
 ; CURRENT FILING DATE: 2002-02-11
 ; PRIOR APPLICATION NUMBER: US 60/267,408
 ; PRIOR FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 638
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 352
 ; LENGTH: 62
 ; TYPE: PRT
 ; ORGANISM: Conus aulicus
 US-10-072-602B-352

Query Match 100.0%; Score 79; DB 14; Length 62;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVCCGYKLCFPC 12
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 Db 50 SVCCGYKLCFPC 61

RESULT 3
 US-10-072-602B-529
 ; Sequence 529, Application US/10072602B
 ; Publication No. US20030109670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: McIntosh, J, Michael
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Cruz, Lourdes J.
 ; APPLICANT: Grilley, Michelle
 ; APPLICANT: Schoenfeld, Robert M.
 ; APPLICANT: Walker, Craig
 ; APPLICANT: Shetty, Reshma
 ; APPLICANT: Jones, Robert M.
 ; TITLE OF INVENTION: Cone Snail Peptides
 ; FILE REFERENCE: 2314-249
 ; CURRENT APPLICATION NUMBER: US/10/072,602B
 ; CURRENT FILING DATE: 2002-02-11
 ; PRIOR APPLICATION NUMBER: US 60/267,408
 ; PRIOR FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 638
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 529
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Conus marmoreus
 US-10-072-602B-529

Query Match 87.3%; Score 69; DB 14; Length 13;
 Best Local Similarity 90.9%; Pred. No. 0.007;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VCCGYKLCFPC 12
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 Db 3 VCCGYKLCFPC 13

RESULT 4
 US-10-072-602B-330
 ; Sequence 330, Application US/10072602B
 ; Publication No. US20030109670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: McIntosh, J, Michael
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Cruz, Lourdes J.
 ; APPLICANT: Grilley, Michelle
 ; APPLICANT: Schoenfeld, Robert M.
 ; APPLICANT: Walker, Craig
 ; APPLICANT: Shetty, Reshma
 ; APPLICANT: Jones, Robert M.
 ; TITLE OF INVENTION: Cone Snail Peptides
 ; FILE REFERENCE: 2314-249
 ; CURRENT APPLICATION NUMBER: US/10/072,602B
 ; CURRENT FILING DATE: 2002-02-11
 ; PRIOR APPLICATION NUMBER: US 60/267,408
 ; PRIOR FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 638
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 330
 ; LENGTH: 61
 ; TYPE: PRT
 ; ORGANISM: Conus marmoreus
 US-10-072-602B-330

Query Match 87.3%; Score 69; DB 14; Length 61;
 Best Local Similarity 90.9%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VCCGYKLCFPC 12
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 Db 51 VCCGYKLCFPC 61

RESULT 5
 US-10-072-602B-345
 ; Sequence 345, Application US/10072602B
 ; Publication No. US20030109670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: McIntosh, J, Michael
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Cruz, Lourdes J.
 ; APPLICANT: Grilley, Michelle
 ; APPLICANT: Schoenfeld, Robert M.
 ; APPLICANT: Walker, Craig
 ; APPLICANT: Shetty, Reshma
 ; APPLICANT: Jones, Robert M.
 ; TITLE OF INVENTION: Cone Snail Peptides
 ; FILE REFERENCE: 2314-249
 ; CURRENT APPLICATION NUMBER: US/10/072,602B
 ; CURRENT FILING DATE: 2002-02-11
 ; PRIOR APPLICATION NUMBER: US 60/267,408
 ; PRIOR FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 638


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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 345
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Conus marmoreus
US-10-072-602B-345

Query Match
Best Local Similarity 86.1%; Score 68; DB 14; Length 61;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VCCGYKLCFPC 12
DB 51 VCCGYKLCCHPC 61

RESULT 6
US-10-072-602B-524
; Sequence 524, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 524
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Conus bandanus
US-10-072-602B-524

Query Match
Best Local Similarity 79.7%; Score 63; DB 14; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGYKLCFPC 12
DB 2 CCGYKLCSPC 11

RESULT 8
US-10-072-602B-527
; Sequence 527, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 527
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Conus pennaceus
US-10-072-602B-527

Query Match
Best Local Similarity 79.7%; Score 63; DB 14; Length 12;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVCCGYKLCFPC 12
DB 1 STCCGFKMCIPC 12

RESULT 9
US-10-072-602B-528
; Sequence 528, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
```

```

; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 528
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Conus episcopatus
US-10-072-602B-528

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Query Match          79.7%; Score 63; DB 14; Length 12;
Best Local Similarity 66.7%; Pred. No. 0.045; 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2;

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QY 1 SVCCGYKLCFPC 12
Db 1 STCCGYRMCVPC 12

```

```

RESULT 10
US-10-072-602B-525
; Sequence 525, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 525
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Conus pennaceus
US-10-072-602B-525

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Query Match          79.7%; Score 63; DB 14; Length 13;
Best Local Similarity 66.7%; Pred. No. 0.045; 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2;

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QY 1 SVCCGYKLCFPC 12
Db 1 STCCGYRMCVPC 12

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RESULT 11
US-10-072-602B-526
; Sequence 526, Application US/10072602B

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; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 526
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Conus pennaceus
US-10-072-602B-526

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Query Match          79.7%; Score 63; DB 14; Length 13;
Best Local Similarity 66.7%; Pred. No. 0.045; 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2;

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QY 1 SVCCGYKLCFPC 12
Db 1 STCCGYRMCVPC 12

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RESULT 12
US-10-072-602B-535
; Sequence 535, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 535
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Conus textile
US-10-072-602B-535

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Query Match          79.7%; Score 63; DB 14; Length 13;
Best Local Similarity 72.7%; Pred. No. 0.045; 1; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2;

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QY 2 VCCGYKLCFPC 12

```

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Db          3 VCCGYRMCVPC 13
|||||:|:|
Query Match      79.7%; Score 63; DB 14; Length 13;
Best Local Similarity 66.7%; Pred. No. 0.045;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 13
US-10-072-602B-538
; Sequence 538, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 538
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Conus pennaceus
US-10-072-602B-538

Query Match      79.7%; Score 63; DB 14; Length 13;
Best Local Similarity 66.7%; Pred. No. 0.045;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY          1 SVCCGYKLCFPC 12
|:|:|:|
Db          1 STCCGFKMCIPC 12

RESULT 14
US-10-072-602B-355
; Sequence 355, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 355
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Conus textile

US-10-072-602B-355
|||||:|:|
Query Match      79.7%; Score 63; DB 14; Length 16;
Best Local Similarity 72.7%; Pred. No. 0.053;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          2 VCCGYKLCFPC 12
|:|:|:|
Db          5 VCCGYRMCVPC 15

RESULT 15
US-10-072-602B-62
; Sequence 62, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Conus bandanus
US-10-072-602B-62

Query Match      79.7%; Score 63; DB 14; Length 61;
Best Local Similarity 90.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY          3 CCGYKLCFPC 12
|:|:|:|
Db          52 CCGYKLCSPC 61

Search completed: August 10, 2004, 16:13:54
Job time : 13.1351 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:00:00 ; Search time 3.72973 Seconds
(without alignments)
309.486 Million cell updates/sec

Title: US-10-072-602B-534
Perfect score: 79
Sequence: 1 SVCCGYKLCFPC 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	67.1	258	T30368	probable immediate
2	50	63.3	55	S25774	testis-specific pr
3	50	63.3	514	T10559	hypothetical prote
4	49	62.0	428	T46025	hypothetical prote
5	47	59.5	245	T10407	immediate early pr
6	47	59.5	373	T47488	hypothetical prote
7	47	59.5	470	C86256	hypothetical prote
8	47	59.5	525	T10574	hypothetical prote
9	44	55.7	342	F64141	probable L-iditol
10	44	55.7	361	T12543	hypothetical prote
11	43	54.4	78	T50943	probable ferredoxi
12	43	54.4	186	A45910	ultra-high-sulfur
13	43	54.4	222	T47487	hypothetical prote
14	43	54.4	373	E84647	hypothetical prote
15	43	54.4	484	T20254	hypothetical prote
16	43	54.4	659	T01520	hypothetical prote
17	42	53.2	350	G84647	hypothetical prote
18	42	53.2	434	A43252	probable transcrip
19	42	53.2	512	F86193	hypothetical prote
20	42	53.2	658	F85024	probable CHP-rich
21	42	53.2	715	S77439	hypothetical prote
22	41	51.9	69	A96696	protein FlN21.2 [i
23	41	51.9	137	G96779	probable RING zinc
24	41	51.9	193	T09043	hypothetical prote
25	41	51.9	226	E86326	protein Fl8014.3 [
26	41	51.9	227	T02413	probable RING zinc
27	41	51.9	235	T19328	hypothetical prote
28	41	51.9	249	T52142	RING finger protei
29	41	51.9	264	T08939	RING zinc finger p

ALIGNMENTS

RESULT 1

T30368

Probable immediate-early transactivator 0 - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T30368
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
Virolology 253, 17-34, 1999

A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d
A:Reference number: Z20836; MUID:99124785; PMID:9887315

A:Accession: T30368

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-258 <KUZ>

A:Cross-references: EMBL:AF081810; PIDN:AC70206.1

C:Keywords: immediate-early protein

Query Match 67.1%; Score 53; DB 2; Length 258;
Best Local Similarity 58.3%; Pred. No. 1.7;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVCCGYKLCFPC 12
DB 207 NVCCGYRVCNAC 218

RESULT 2

S25774

testis-specific protein Mst84Dc - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999

C:Accession: S25774; C56565

R:Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.

Mech. Dev. 35, 143-151, 1991

A:Title: A cluster of four genes selectively expressed in the male germ line of Drosophi
A:Reference number: A56565; MUID:92102953; PMID:1684716

A:Accession: S25774

A:Molecule type: DNA

A:Residues: 1-55 <KUH>

A:Cross-references: EMBL:X67703; NID:g11072; PIDN:CAA47939.1; PID:g11075

A>Note: the authors translated the codon TGC for residue 55 as Thr

C:Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBI:74222)

C:Genetics:

A:Gene: Mst84DC

A:Cross-references: FlyBase:FBgn0004174

A:Map position: 3

C:Superfamily: fruit fly testis-specific protein

C:Keywords: spermatogenesis; tandem repeat

Query Match 63.3%; Score 50; DB 2; Length 55;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCGYKLCFPC 12
|||||
Db 9 CCGYCCGPC 18

RESULT 3

T10559
hypothetical protein F25E4.10 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C:Accession: T10559
R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft, R.; et al.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16533
A:Accession: T10559
A:Molecule type: DNA
A:Residues: 1-514 <BEV>
A:Cross-references: EMBL:AL050399; GSPDB:GN00062; ATSP:F25E4.10
A:Experimental source: cultivar Columbia; BAC clone F25E4
C:Genetics:
A:Gene: ATSP:F25E4.10
A:Map position: 4
A:Introns: 436/3; 457/3; 479/3

Query Match 63.3%; Score 50; DB 2; Length 514;
Best Local Similarity 70.0%; Pred. No. 7.3;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGYKLCFPC 12
|||||
Db 295 CCGFVLCFCC 304

RESULT 4

T46025
hypothetical protein T10K17.240 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
C:Accession: T46025
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F. et al.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23019
A:Accession: T46025
A:Molecule type: DNA
A:Residues: 1-428 <BEN>
A:Cross-references: EMBL:AL132977
A:Experimental source: cultivar Columbia; BAC clone T10K17
C:Genetics:
A:Map position: 3
A:Note: T10K17.240
C:Superfamily: RING finger homology
F127-176/Domain: RING finger homology <RRN>

Query Match 62.0%; Score 49; DB 2; Length 428;
Best Local Similarity 60.0%; Pred. No. 8.8;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGYKLCFPC 12
|||||
Db 145 CCGHLYCWPC 154

RESULT 5

T10407
immediate early protein 0 - Orgyia pseudotsugata nuclear polyhedrosis virus
C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C:Accession: T10407
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis

A:Reference number: Z17011; MUID:97271300; PMID:9126251
A:Accession: T10407
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-245 <AHR>
A:Cross-references: EMBL:U75930; NID:g2934903; PID:g1911384

Query Match 59.5%; Score 47; DB 2; Length 245;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCGYKLCFPC 12
|||||
Db 213 CCGYSLCYAC 222

RESULT 6

T47488
hypothetical protein F9K21.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47488
R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.; et al.
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24467
A:Accession: T47488
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-373 <JOR>
A:Cross-references: EMBL:AL138657
A:Experimental source: cultivar Columbia; BAC clone F9K21
C:Genetics:
A:Map position: 3
A:Introns: 92/3; 328/2; 353/3
A:Note: F9K21.60

Query Match 59.5%; Score 47; DB 2; Length 373;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGYKLCFPC 12
|||||
Db 329 CCGYKFCYAC 337

RESULT 7

C86256
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86256
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; et al.
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; et al.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; et al.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, R.; et al.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; et al.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86256
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <STO>
A:Cross-references: GB:AE005172; NID:gl0086520; PIDN:AA012580.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 59.5%; Score 47; DB 2; Length 470;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGYKLCFP 11
| | | | |
DB 283 CTGYKYCFF 291

RESULT 8

T10574
hypothetical protein F25E4.160 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C:Accession: T10574
R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16533
A:Accession: T10574
A:Molecule type: DNA
A:Residues: 1-525 <BEV>
A:Cross-references: EMBL:AL050399; GSPDB:GN00062; ATSP:F25E4.160
A:Experimental source: cultivar Columbia; BAC clone F25E4
C:Genetics:
A:Gene: ATSP:F25E4.160
A:Map position: 4

Query Match 59.5%; Score 47; DB 2; Length 525;

Best Local Similarity 77.8%; Pred. No. 19; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGYKLCFP 12
| | | | |
DB 433 CCGYKLCFP 441

RESULT 9

F64141
probable L-iditol 2-dehydrogenase (EC 1.1.1.14) HI0053 - Haemophilus influenzae (strain N)
A:Alternate names: sorbitol dehydrogenase
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 11-Jun-1999
C:Accession: F64141
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kierlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: F64141
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-342 <TIGR>
A:Cross-references: GB:U32690; GB:L42023; NID:g1572991; PIDN:AAC21731.1; PID:g1573000; T

C:Function:
A:Description: catalyzes the oxidation by NAD+ of sorbitol to fructose
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: metalloprotein; NAD; oxidoreductase; zinc
F:26-331/Domain: long-chain alcohol dehydrogenase homology <LADH>
F:168-197/Region: beta-alpha-beta NAD nucleotide-binding fold
F:41,63,149/Binding site: zinc, catalytic (Cys, His, Glu) #status predicted
F:94,97,100,108/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match 55.7%; Score 44; DB 1; Length 342;

Best Local Similarity 63.6%; Pred. No. 38; Mismatches 7; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 2 VCCGYKLCFP 12
| | | | |
DB 92 VCCGYKLCFP 100

RESULT 10

T12543
hypothetical protein DKFZp434M154.1 - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: T12543
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17524
A:Accession: T12543
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-361 <WAM>
A:Cross-references: EMBL:AL080159
A:Experimental source: adult testis; clone DKFZp434M154
C:Genetics:
A:Note: DKFZp434M154.1

Query Match 55.7%; Score 44; DB 2; Length 361;

Best Local Similarity 75.0%; Pred. No. 39; Mismatches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GYKLCFP 12
| | | | |
DB 300 GHKFCFP 307

RESULT 11

T50943
probable ferredoxin Dita [imported] - Pseudomonas abietaniphila

C:Species: Pseudomonas abietaniphila
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50943
R:Martin, V.J.; Mohn, W.W.
J. Bacteriol. 181, 2675-2682, 1999
A:Title: A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-degrading
A:Reference number: Z25281; MUID:99235742; PMID:10217753
A:Accession: T50943
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-78 <VAR>

A:Cross-references: EMBL:AF119621; PIDN:AAD21062.1

A:Experimental source: strain BKME-9; ATCC700689

C:Genetics:

A:Gene: dita3

Query Match 54.4%; Score 43; DB 2; Length 78;

Best Local Similarity 77.8%; Pred. No. 18; Mismatches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVCCGYKLC 9
| | | | |
DB 15 SRCCGYGLC 23

RESULT 12

A45910

ultra-high-sulfur keratin - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 24-Sep-1999

C:Accession: A45910

R:McNab, A.R.; Wood, L.; Theriault, N.; Gierman, T.; Vogeli, G.

J. Invest. Dermatol. 92, 263-266, 1989

A:Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth.

A:Reference number: A45910; MUID:89140394; PMID:2465353

A:Accession: A45910

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-186 <MCN>

A:Cross-references: GB:M27685; NID:g341749; PIDN:AAA81560.1; PID:g1066818

C:Superfamily: ultra-high-sulfur keratin

Query Match

54.4%; Score 43; DB 2; Length 186;

Best Local Similarity 60.0%; Pred. No. 34;

Mismatches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CCGYKLCFPC 12
 ||| |
 Db 42 CCGSSCCQPC 51

RESULT 13

T47487

hypothetical protein F9K21.50 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T47487
 R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.

A:Reference number: Z24467
 A:Accession: T47487
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-222 <OR>
 A:Cross-references: EMBL:AL138657
 A:Experimental source: cultivar Columbia; BAC clone F9K21
 C:Genetics:
 A:Map position: 3
 A:Introns: 186/2
 A:Note: F9K21.50

Query Match 54.4%; Score 43; DB 2; Length 222;
 Best Local Similarity 55.6%; Pred. No. 38;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGYKLCFPC 12
 ||| |
 Db 187 CGYQFCYKC 195

Search completed: August 10, 2004, 16:04:57
 Job time : 4.72973 secs

RESULT 14

E84647

hypothetical protein At2g25360 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: E84647
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84647
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-373 <STO>
 A:Cross-references: GB:AE002093; NID:94432849; PIDN:AAD20697.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g25360
 A:Map position: 2

Query Match 54.4%; Score 43; DB 2; Length 373;
 Best Local Similarity 55.6%; Pred. No. 55;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGYKLCFPC 12
 ||| |
 Db 273 CGYQFCYQC 281

RESULT 15

T20254

hypothetical protein C55A6.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
 C:Accession: T20254
 R:Kerhaw, J.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19243

A:Accession: T20254
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-484 <WIL>
 A:Cross-references: EMBL:Z81051; PIDN:CAB02861.1; GSPDB:GN00023; CESP:C55A6.1
 A:Experimental source: clone C55A6
 C:Genetics:
 A:Gene: CESP:C55A6.1
 A:Map position: 5
 A:Introns: 84/1; 102/1; 220/3; 275/1; 298/3; 331/2; 464/3
 C:Superfamily: RING finger homology
 F:8-57/Domain: RING finger homology <RRN>

Query Match 54.4%; Score 43; DB 2; Length 484;
 Best Local Similarity 66.7%; Pred. No. 66;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGYKLCFPC 12
 ||| |
 Db 28 CGHKFCFC 36

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 15:56:10 ; Search time 2.59459 Seconds
(without alignments)
240.824 Million cell updates/sec

Title: US-10-072-602b-534
Perfect score: 79
Sequence: 1 SVCCGYKLCFPC 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	68	86.1	11	1	CXL1_CONMR
2	68	86.1	13	1	CXL4_CONMR
3	68	86.1	61	1	CXL2_CONMR
4	54	68.4	12	1	CXL3_CONMR
5	50	63.3	55	1	M84C_DROME
6	47	59.5	245	1	IEO_NPVOP
7	44	55.7	342	1	Y053_HAEIN
8	44	55.7	503	1	ARI1_DROME
9	42.5	53.8	30	1	CRX4_CONST
10	42	53.2	434	1	ADA2_YEAST
11	41	51.9	235	1	YQ57_CABEL
12	41	51.9	539	1	RN37_MOUSE
13	41	51.9	541	1	RN37_HUMAN
14	41	51.9	1885	1	RRPO_ACLS
15	40	50.6	207	1	CSF3_HUMAN
16	40	50.6	452	1	RN18_HUMAN
17	40	50.6	566	1	IRL1_RAT
18	40	50.6	567	1	IRYU_MOUSE
19	40	50.6	575	1	Y0Y6_CABEL
20	40	50.6	4655	1	LRP2_HUMAN
21	39.5	50.0	1984	1	YL_DROME
22	39	49.4	208	1	CSF3_MOUSE
23	39	49.4	257	1	RFBF_SALTY
24	39	49.4	400	1	VG78_HSV1
25	39	49.4	459	1	ARI1_MOUSE
26	39	49.4	467	1	ARI1_HUMAN
27	39	49.4	4543	1	LRP1_CHICK
28	39	49.4	4544	1	LRP1_HUMAN
29	38.5	48.7	92	1	NEO2_LOXAF
30	38.5	48.7	6781	1	R1AB_PEDV7
31	38	48.1	72	1	YVAU_VACCC
32	38	48.1	232	1	SLT2_CABEL
33	38	48.1	261	1	IEO_NPVAC

34	38	48.1	274	1	YEUS_YEAST	P40072	saccharomyc
35	38	48.1	321	1	ABNA_ASPNG	P42556	aspergillus
36	38	48.1	399	1	PEXC_YEAST	Q04370	saccharomyc
37	38	48.1	408	1	VIEN_NPVAC	P24647	autographa
38	38	48.1	461	1	PRTC_HUMAN	P04070	homo sapien
39	38	48.1	584	1	POTE_HUMAN	Q86YR6	homo sapien
40	38	48.1	653	1	HT2A_HUMAN	Q13049	homo sapien
41	38	48.1	685	1	MID2_MOUSE	Q9QUS6	mus musculus
42	38	48.1	715	1	MID2_HUMAN	Q9UJV3	homo sapien
43	38	48.1	775	1	CN04_MOUSE	Q8K3X4	mus musculus
44	38	48.1	796	1	CN04_HUMAN	Q9H1B7	homo sapien
45	38	48.1	872	1	MGR2_HUMAN	Q14416	homo sapien

ALIGNMENTS

```
RESULT 1
CXL1_CONMR
ID_CXL1_CONMR STANDARD; PRT; 11 AA.
AC P58807;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CMrVIA.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20564325; PubMed=10988292;
RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA Seow K.T., Bay B.-H.;
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT pattern and protein folding. Isolation and characterization from the
RT venom of Conus marmoreus."
RL J. Biol. Chem. 275:39516-39522(2000).
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
CC -!- SIMILARITY: belongs to the chi/lambda-conotoxin family.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 2 11
FT DISULFID 3 8
FT MOD_RES 10 10 HYDROXYLATION.
FT SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;
Query Match 86.1%; Score 68; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 VCCGYKLCFPC 12
DB 1 VCCGYKLCFPC 11
RESULT 2
CXL4_CONMR STANDARD; PRT; 13 AA.
ID_CXL4_CONMR
AC P58810;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda/chi-conotoxin Mr1B (Chi-Mr1B).
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
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RN  [1]
RP  SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
RC  TISSUE=Venom;
RX  MEDLINE=21419681; PubMed=11528421;
RA  Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
RA  Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
RA  Lewis R.J.;
RT  "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
RT  noradrenaline transporter.";
RL  Nat. Neurosci. 4:902-907(2001).
CC  -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -!- PTM: Exists in two forms, due to cis-trans isomerization at His-
CC  11-Hyp-12.
CC  -!- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
CC  -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
DR  PDB; 1IB0; 03-APR-02.
KW  Neurotoxin; Toxin; Hydroxylation; 3D-structure.
FT  DISULFID 4 13
FT  DISULFID 5 10
FT  MOD_RES 12 12
FT  SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;
SQ  QUERY Match 86.1%; Score 68; DB 1; Length 13;
    Best Local Similarity 90.9%; Pred. No. 0.00015;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 VCCGYKLCFPC 12
DB  3 VCCGYKLCFPC 13

RESULT 3
CXL2_CONMR
ID  CXL2_CONMR STANDARD; PRT; 61 AA.
AC  P5808;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Lambda-conotoxin CMrVB precursor (Chi-conotoxin Mr1A) (Chi-Mr1A)
DE  (Mr10a).
OS  Conus marmoreus (Marble cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=42752;
RN  [1]
RP  SEQUENCE FROM N.A., SEQUENCE OF 49-61, SYNTHESIS, AND MASS
RP  SPECTROMETRY.
RC  TISSUE=Venom, and Venom duct;
RX  MEDLINE=20490660; PubMed=10900201;
RA  McIntosh J.M., Corpuz G.O., Layer R.T., Garrett J.E., Wagstaff J.D.,
RA  Bula J.G., Vyazovkina A., Yoshikami D., Cruz L.J., Olivera B.M.;
RT  "Isolation and characterization of a novel conus peptide with apparent
RT  antinociceptive activity.";
RL  J. Biol. Chem. 275:32391-32397(2000).
RN  [2]
RP  SEQUENCE OF 49-61, AND MASS SPECTROMETRY.
RC  TISSUE=Venom;
RX  MEDLINE=20564325; PubMed=10988292;
RA  Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA  Seow K.T., Bay B.-H.;
RT  "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT  pattern and protein folding. Isolation and characterization from the
RT  venom of Conus marmoreus.";
RL  J. Biol. Chem. 275:39516-39522(2000).
RN  [3]
RP  SEQUENCE OF 49-61, SYNTHESIS, MASS SPECTROMETRY, AND STRUCTURE BY NMR.
RC  TISSUE=Venom;
RX  MEDLINE=21419681; PubMed=11528421;
RA  Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
RA  Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,

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RA  Lewis R.J.;
RT  "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
RT  noradrenaline transporter.";
RL  Nat. Neurosci. 4:902-907(2001).
CC  -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -!- PTM: Exists in two forms, due to cis-trans isomerization at His-
CC  59-Hyp-60.
CC  -!- MASS SPECTROMETRY: MW=1408.5; METHOD=Electrospray.
CC  -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
DR  InterPro; IPR004214; Conotoxin.
KW  Neurotoxin; Toxin; Hydroxylation; Signal.
FT  SIGNAL 1 19
FT  PROPEP 20 48
FT  PEPTIDE 49 61
FT  DISULFID 52 61
FT  DISULFID 53 58
FT  MOD_RES 60 60
FT  SEQUENCE 61 AA; 6499 MW; F4DESB5A97EB8DBA CRC64;
SQ  QUERY Match 86.1%; Score 68; DB 1; Length 61;
    Best Local Similarity 90.9%; Pred. No. 0.0006;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 VCCGYKLCFPC 12
DB  51 VCCGYKLCFPC 61

RESULT 4
CXL3_CONMR
ID  CXL3_CONMR STANDARD; PRT; 12 AA.
AC  P5809;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Lambda-conotoxin CMrX.
OS  Conus marmoreus (Marble cone).
OC  Apogastropoda; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=42752;
RN  [1]
RP  SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC  TISSUE=Venom;
RX  MEDLINE=20564325; PubMed=10988292;
RA  Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA  Seow K.T., Bay B.-H.;
RT  "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT  pattern and protein folding. Isolation and characterization from the
RT  venom of Conus marmoreus.";
RL  J. Biol. Chem. 275:39516-39522(2000).
CC  -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -!- MASS SPECTROMETRY: MW=1262.77; MW ERR=0.07; METHOD=Electrospray.
CC  -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
KW  Neurotoxin; Toxin; Hydroxylation.
FT  DISULFID 3 12
FT  DISULFID 4 9
FT  MOD_RES 11 11
FT  SEQUENCE 12 AA; 1251 MW; 277AAE2422DSA2C8 CRC64;
SQ  QUERY Match 68.4%; Score 54; DB 1; Length 12;
    Best Local Similarity 54.5%; Pred. No. 0.016;
    Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  2 VCCGYKLCFPC 12
DB  2 ICCGVSCFPC 12

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--!- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
CC

RESULT 8

development, with maximum levels reached during metamorphosis and maintained in the adult.

CC -!- SIMILARITY: Contains 2 RING-type zinc fingers.
 CC -!- SIMILARITY: Contains 1 IBR-type zinc finger.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; X98309; CAA66953.1; -;
 DR EMBL; X98310; CAA66954.1; -;
 DR FLYBase; AE003507; AAF48807.1; -;
 DR FLYBase; FBGN017418; ari-1.
 DR InterPro; IPR002867; Znf_CGHC.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF01485; IBR; 1.
 DR SMART; SM00647; IBR; 2.
 DR SMART; SM00184; RING; 2.
 DR PROSITE; PS00518; 2F_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; 2F_RING_2; 1.
 KW Ubl conjugation pathway; Zinc-finger; Repeat; Coiled coil.
 FT DOMAIN 22 27 ASP-RICH (ACIDIC).
 FT ZN_FING 133 182 RING-TYPE 1.
 FT ZN_FING 203 264 IBR-TYPE.
 FT ZN_FING 291 336 RING-TYPE 2.
 FT DOMAIN 133 201 INTERACTION WITH UBQD10.
 FT DOMAIN 341 361 COILED COIL (POTENTIAL).
 FT MUTAGEN 150 150 LOSS OF INTERACTION WITH UBQD10.
 FT C->Y: IN AR11-2; LETHAL PHENOTYPE AND
 FT C->Y: IN AR11-3; LETHAL PHENOTYPE AND NO
 FT LOSS OF INTERACTION WITH UBQD10.
 FT SEQUENCE 503 AA; 58932 MW; 08ECCE256CF5EC00 CRC64;
 Query Match 55.7%; Score 44; DB 1; Length 503;
 Best Local Similarity 55.6%; Pred. No. 14;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CC 4 CGYKLCFPC 12
 Db 150 CGHRCFPC 158

RESULT 9
 CXK4_CONST
 ID_CXK4_CONST STANDARD; PRT; 30 AA.
 AC PS8921;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Kappa-A-conotoxin SIVA (Spastic peptide).
 OS Conus striatus (Striated cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Neogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6493;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=99036623; PubMed=9819194;
 RA Craig A.G., Zafaralla G.C., Cruz L.J., Santos A.D., Hillyard D.R.,
 RA Dykert J., Rivier J.E., Gray W.R., Imperial J.S., Delacruz R.G.,
 RA Sporning A., Terlau H., West P.J., Yoshikami D., Olivera B.M.;
 RT "An O-Glycosylated neuroexcitatory conus peptide.";
 RL Biochemistry 37:16019-16025(1998).
 CC -!- FUNCTION: Kappa-A-conotoxins bind and inhibit voltage-sensitive
 CC potassium channels. When injected intraperitoneally in fish, the
 CC peptide induces a period of rapid swimming followed by a spastic
 CC paralysis with stiff fibrillating fins. At high doses, the peptide
 CC is lethal to both fish and mice.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- PTM: O-linked glycan consists of Hex3-HexNAc2 disaccharide
 CC (Probable).

CC -!- MASS SPECTROMETRY: MW=4084.2; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily.
 KW Toxin; Neurotoxin; Ionic channel inhibitor;
 KW Potassium channel inhibitor; Hydroxylation; Amidation;
 KW Pyrrolidone carboxylic acid; Glycoprotein.
 FT DISULFID 12 24 PROBABLE.
 FT DISULFID 13 26 PROBABLE.
 FT DISULFID 21 30 PROBABLE.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 7 7 O-LINKED.
 FT MOD_RES 17 17 HYDROXYLATION.
 FT MOD_RES 22 22 HYDROXYLATION.
 FT MOD_RES 23 23 HYDROXYLATION.
 FT MOD_RES 30 30 AMIDATION.
 SQ SEQUENCE 30 AA; 3166 MW; 758A8CCLF146D7D5 CRC64;

Query Match 53.8%; Score 42.5; DB 1; Length 30;
 Best Local Similarity 46.7%; Pred. No. 1.8;
 Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

CC 1 SVCCGY---KLCPFC 12
 Db 10 TTCGYDPGTMCPPC 24

RESULT 10
 ADA2 YEAST
 ID_ADA2 YEAST STANDARD; PRT; 434 AA.
 AC Q02336;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Transcriptional adaptor 2.
 GN ADA2 OR YDR448W OR D9461.33.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92346713; PubMed=1638630;
 RA Berger S.L., Pina B., Silverman N., Marcus G.A., Agapite J.,
 RA Regier J.L., Triebenberg S.J., Guarente L.;
 RT "Genetic isolation of ADA2: a potential transcriptional adaptor
 RT required for function of certain acidic activation domains.";
 RL Cell 70:251-265(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97313263; PubMed=9169867;
 RA Jacq C., Alt-Moerbe J., Andre B., Arnold W., Bahr A., Ballesta J.P.G.,
 RA Barques M., Baron L., Becker A., Biteau N., Bloeker H., Blugson C.,
 RA Boskovic J., Brand P., Brueckner M., Butrago M.J., Coster F.,
 RA Delaveau T., Del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,
 RA Goifeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T.,
 RA Hoheisel J.D., Jaeger W., Jimenez A., Joniaux J.-L., Kraemer C.,
 RA Kuester H., Laamanen P., Legros Y., Louis E.J., Moeller-Rieker S.,
 RA Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,
 RA Paulin L., Perea J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,
 RA Prydz H., Fumelle B., Rasmussen S.W., Remacha M., Revuelta J.L.,
 RA Rieger M., Salom D., Saluz H.P., Saiz J.E., Saren A.-M., Schaefer M.,
 RA Scharfe M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,
 RA Urrestarazu L.A., Verhasselt P., Vissers S., Voet M., Voickaert G.,
 RA Wagner G., Wambutt R., Wedler E., Wieders H., Woelfl S., Harris D.E.,
 RA Bowman S., Brown D., Churcher C.M., Connor R., Dedman K., Gentles S.,
 RA Hamlin N., Hunt S., Jones L., McDonald S., Murphy L., Niblett D.,
 RA Odel C., Oliver K., Rajandream M.A., Richards C., Shore L.,
 RA Walsh S.V., Barrell B.G., Dietrich F.S., Mulligan J.T., Allen E.,
 RA Araujo R., Aviles E., Bero A., Carpenter J., Chen E., Cherry J.M.,
 RA Chung E., Duncan M., Hunnicke-Smith S., Hyman R.W., Komp C.,

RA Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A.,
 RA Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M.,
 RA Shogren T., Shroff N., Winant A., Yelton M.A., Botstein D.,
 RA Davis R.W., Johnston M., Andrews S., Brinkman R., Cooper J., Ding H.,
 RA Du Z., Favell A., Fulton L., Gattung S., Greco T., Hallsworth K.,
 RA Hawkins J., Hillier L.W., Jier M., Johnson D., Johnston L.,
 RA Kirsten J., Kucaba T., Langston Y., Latreille P., Le T., Mardis E.,
 RA Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifkin L.,
 RA Riles L., Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P.,
 RA Vaudin M., Wilson R., Waterston K., Albermann K., Hani J., Heumann K.,
 RA Kleine K., Mewes H.-W., Zollner A., Zaccaria P.;
 RT "the nucleotide sequence of *Saccharomyces cerevisiae* chromosome IV.";
 RL Nature 387:75-78(1997).
 RN [3]
 RN ASSOCIATION WITH GCN5.
 RP MEDLINE=95045371; PubMed=7957049;
 RX Marcus G.A., Silverman N., Berger S.L., Horiuchi J., Guarente L.;
 RA "Functional similarity and physical association between GCN5 and
 RT ADA2: putative transcriptional adaptors.";
 RL EMBO J. 13:4807-4815(1994).
 RN [4]
 RN IDENTIFICATION IN A SAGA COMPLEX WITH SPT7; HFI1; SPT8; GCN5; SPT20;
 RP SPT2; ADA3 AND TRAI.
 RX MEDLINE=99102959; PubMed=9885573;
 RA Grant P.A., Schielfz D., Pray-Grant M.G., Yates J.R. III,
 RA Workman J.L.;
 RT "The ATM-related cofactor Tral is a component of the purified SAGA
 RT complex.";
 RL Mol. Cell 2:863-867(1998).
 CC -1- FUNCTION: Required for the function of some acidic activation
 CC domains, which activate transcription from a distant site. The
 CC exact mechanism of action is not yet known. ADA2, ADA3 and GCN5
 CC function to acetylate nucleosomes opening up the promoter region.
 CC -1- SUBUNIT: Interacts with GCN5. Part of the ADA/GCN5 complex that
 CC consists of HFI1/ADA1, ADA2, ADA3, SPT20/ADA5 and GCN5. Component
 CC of the SAGA complex, a large multiprotein complex that modifies
 CC the chromatin, at least composed of SPT2, SPT7, SPT8, SPT20/ADA5,
 CC HFI1, ADA2, ADA3/NGI1, TRAI and GCN5.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: Contains 1 Myb-like domain.
 CC -1- SIMILARITY: Contains 1 SWIRM domain.
 CC -1- SIMILARITY: Contains 1 ZZ-type zinc finger.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M95396; AAA34393.1; -;
 CC EMBL; U33007; AAB64871.1; -;
 CC PIR; A43252; A43252.
 CC GenOnline; 140940; -;
 CC TRANSFAC; T02144; -;
 CC SGD; S0002856; ADA2.
 CC GO; GO:0000124; C:SAGA complex; IDA.
 CC InterPro; IPR001005; Myb DNA binding.
 CC InterPro; IPR007526; SWIRM.
 CC InterPro; IPR000433; Znf ZZ.
 CC Pfam; PF00249; myb_DNA-binding; 1.
 CC Pfam; PF04433; SWIRM; 1.
 CC Pfam; PF00569; ZZ; 1.
 CC SMART; SM00717; SANT; 1.
 CC SMART; SM00291; Znf ZZ; 1.
 CC PROSITE; PS00037; MYB_1; FALSE_NEG.
 CC PROSITE; PS00334; MYB_2; FALSE_NEG.
 CC PROSITE; PS00900; MYB_3; 1.
 CC PROSITE; PS00934; SWIRM; 1.
 CC PROSITE; PS01357; ZF_ZZ_1; 1.
 CC PROSITE; PS01355; ZF_ZZ_2; 1.
 CC Transcription regulation; Nuclear protein; Zinc-finger.

FT ZN FING 1 48 ZZ-TYPE.
 FT DNA_BIND 65 108 MYB.
 FT DOMAIN 349 434 SWIRM.
 SQ SEQUENCE 434 AA; 50569 MW; 9637E1EDBBED0AC3 CRC64;
 Query Match 53.2%; Score 42; DB 1; Length 434;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SVCCGYKLCFPC 12
 Db 23 AICPEYDLVCVC 34
 RESULT 11
 YQ57_CAEEL STANDARD; PRT; 235 AA.
 ID YQ57_CAEEL
 AC Q09463;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical RING finger protein Cl6C10.7 in chromosome III.
 GN Cl6C10.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RC Lloyd C.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC -----
 CC EMBL; Z46787; CAA86745.1; -;
 CC PIR; T19328; T19328.
 CC WormPep; Cl6C10.7; CE01498.
 CC InterPro; IPR001841; Znf_fing.
 CC Pfam; PF00097; zf-G3HC4; 1.
 CC SMART; SM00184; RING; 1.
 CC PROSITE; PS00518; ZF_RING_1; 1.
 CC PROSITE; PS0089; ZF_RING_2; 1.
 CC Hypothetical protein; Zinc-finger.
 KW ZN_FING 26 67 RING-TYPE.
 FT DOMAIN 121 124 POLY-GLY.
 FT DOMAIN 169 172 POLY-ALA.
 SQ SEQUENCE 235 AA; 24915 MW; 21A04AB951F6382A CRC64;
 Query Match 51.9%; Score 41; DB 1; Length 235;
 Best Local Similarity 55.6%; Pred. No. 20;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CGYKLCFPC 12
 Db 41 CGHLFCWPC 49
 RESULT 12
 RN37_MOUSE STANDARD; PRT; 539 AA.
 ID RN37_MOUSE
 AC Q925F4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ring finger protein 37 (Ubiquitin conjugating enzyme 7 interacting

[5] SEQUENCE OF 19-207 FROM N.A.
 RP MEDLINE=86151684; PubMed=2420009;
 RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zeebo K.M.,
 RA Murodock D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,
 RA Barendt J., Platzner E., Moore M.A.S., Mertelsmann R., Welte K.;
 RT "Recombinant human granulocyte colony-stimulating factor: effects on
 RT normal and leukemic myeloid cells.";
 RL Science 232:61-66(1986).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=93293942; PubMed=7685769;
 RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;
 RA "Glycosidase digestion, electrophoresis and chromatographic analysis
 RT of recombinant human granulocyte colony-stimulating factor glycoforms
 RT produced in Chinese hamster ovary cells.";
 RL J. Chromatogr. A 637:55-62(1993).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93106200; PubMed=1281794;
 RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
 RA "Secondary structure of human granulocyte colony-stimulating factor
 RT derived from NMR spectroscopy.";
 RL FEBS Lett. 314:435-439(1992).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94304859; PubMed=7518249;
 RA Zink T., Ross A., Luers K., Gieslar C., Rudolph R., Holak T.A.;
 RA "Structure and dynamics of the human granulocyte colony-stimulating
 RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-
 RT bundle protein.";
 RL Biochemistry 33:8453-8463(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=93281718; PubMed=7685117;
 RA Hill C.P., Osslund T.D., Eisenberg D.;
 RA "The structure of granulocyte-colony-stimulating factor and its
 RT relationship to other growth factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171(1993).
 CC -I- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
 CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
 CC CSF INDUCES GRANULOCYTES.
 CC -I- SUBUNIT: Monomer.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P09919-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P09919-2; Sequence=VSP_002673;
 CC -I- PTM: O-GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH CAN BE
 CC MODIFIED WITH UP TO TWO SIALIC ACID RESIDUES (DONE IN
 CC RECOMBINANTLY EXPRESSED G-CSF FROM CHO CELLS).
 CC -I- PHARMACEUTICAL: Available under the names Neupogen or Granulokine
 CC (Amgen/Roche) and Granocyte (Rhône-Poulenc). Used to treat
 CC neutropenia (a disorder characterized by an extremely low number
 CC of neutrophils in blood).
 CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -I- CAUTION: REF.4 MISQUOTES THE GENE NAME AS "CSF1".
 CC -I- DATABASES: NAME=Neupogen/Granulokine;
 CC NOTE=Clinical information on Neupogen/Granulokine;
 CC WWW="http://www.neupogen.com/".
 CC
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DR EMBL; X03438; CAA27168.1; -;
 DR EMBL; M13008; AAA03056.1; -;
 DR EMBL; X03656; CAA27291.1; -;
 DR EMBL; X03655; CAA27290.1; -;
 DR EMBL; AF388025; AAK62469.1; -;
 DR EMBL; M17706; AAA35882.1; -;
 DR PIR; A24573; A24573;
 DR PIR; A25093; FQHUGL;
 DR PDB; 1RHG; 31-JAN-94.
 DR PDB; 1GNC; 31-JUL-94.
 DR PDB; 1CD9; 08-MAR-00.
 DR PDB; 1PGR; 08-MAR-00.
 DR Genew; HGNC:2438; CSF3.
 DR MIM; 138970; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005130; F:granulocyte colony-stimulating factor recep. .; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 DR InterPro; IPR003629; GCSF_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRODOM; PD008388; GCSF_MGF; 1.
 DR SMART; SM0126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Growth factor; Glycoprotein; Signal; Alternative splicing;
 KW Polymorphism; Pharmaceutical; 3D-structure.
 FT SIGNAL 1 30 GRANULOCYTE COLONY-STIMULATING FACTOR.
 FT CHAIN 31 207
 FT DISULFID 69 75
 FT DISULFID 97 107
 FT CARBOHYD 166 166
 FT VARSPLIC 66 68
 FT VARIANT 157 157
 FT VARIANT 174 174
 FT HELIX 41 65
 FT HELIX 69 71
 FT HELIX 77 86
 FT TURN 87 88
 FT HELIX 105 124
 FT TURN 125 127
 FT TURN 130 132
 FT HELIX 133 156
 FT TURN 157 158
 FT HELIX 176 203
 FT TURN 204 204
 SQ SEQUENCE 207 AA; 22293 MW; 421F635ECC776996 CRC64;
 Query Match 50.6%; Score 40; DB 1; Length 207;
 Best Local Similarity 63.6%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SVCCGKLCPP 11
 Db 67 SECATYKLCPP 77

Search completed: August 10, 2004, 16:03:05
 Job time : 3.59459 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 15:59:20 ; Search time 10.8649 Seconds
(without alignments)
348.483 Million cell updates/sec

Title: US-10-072-602B-534
Perfect score: 79
Sequence: 1 SVCCGYKLCFPC 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp archaea:*
- 2: sp bacteria:*
- 3: sp fungi:*
- 4: sp human:*
- 5: sp invertebrate:*
- 6: sp mammal:*
- 7: sp mhc:*
- 8: sp organelle:*
- 9: sp phage:*
- 10: sp plant:*
- 11: sp rodent:*
- 12: sp virus:*
- 13: sp vertebrate:*
- 14: sp unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	79.7	64	5 Q9BPE9	Q9bpe9 conus penna
2	54	68.4	244	12 Q9IBQ9	Q9ibq9 spodoptera
3	53	67.1	243	12 Q80LS1	Q80ls1 adoxophyes
4	53	67.1	258	12 Q36453	Q36453 lymantria d
5	52	65.8	446	4 Q96BQ3	Q96bq3 homo sapien
6	50	63.3	151	12 Q10614	Q10614 helicoverpa
7	50	63.3	285	12 Q8V5X4	Q8v5x4 helicoverpa
8	50	63.3	285	12 Q99H38	Q99h38 helicoverpa
9	50	63.3	514	10 Q9LD86	Q9ld86 arabidopsis
10	49	62.0	428	10 Q9M2P5	Q9m2p5 arabidopsis
11	49	62.0	436	10 Q8RFX2	Q8rxf2 arabidopsis
12	48	60.8	2259	10 Q7XIF9	Q7xif9 oryza sativ
13	47	59.5	373	10 Q9M1F9	Q9m1f9 arabidopsis
14	47	59.5	470	10 Q9FWW3	Q9fww3 arabidopsis
15	47	59.5	525	10 Q9LE85	Q9le85 arabidopsis
16	47	59.5	641	17 Q9HJH7	Q9hj7 thermoplasm

17	46	58.2	69	2	Q9R5Z5	Q9r625 nocardioid
18	46	58.2	220	5	Q8SUS9	Q8sus9 encephalito
19	46	58.2	234	12	Q8QL66	Q8ql66 mamestra co
20	46	58.2	234	12	Q8JLY7	Q8jly7 mamestra co
21	46	58.2	429	5	Q95V23	Q95v23 drosophila
22	46	58.2	429	5	Q9V9C9	Q9v9c9 drosophila
23	46	58.2	543	10	Q9FLZ0	Q9flz0 arabidopsis
24	45.5	57.6	593	5	Q97226	Q97226 plasmodium
25	45	57.0	47	4	Q9UN35	Q9un35 homo sapien
26	45	57.0	75	4	Q9UHU5	Q9uhu5 homo sapien
27	45	57.0	132	11	Q9CQP5	Q9ccp5 mus musculu
28	45	57.0	167	11	Q9D122	Q9d122 mus musculu
29	45	57.0	168	11	Q9D732	Q9d732 mus musculu
30	45	57.0	171	11	Q8BJ87	Q8bj87 mus musculu
31	45	57.0	176	11	Q8BU09	Q8bu09 mus musculu
32	45	57.0	189	11	Q8BLE9	Q8ble9 mus musculu
33	45	57.0	235	11	Q9D7I0	Q9d7i0 mus musculu
34	45	57.0	235	11	Q8BJ86	Q8bj86 mus musculu
35	45	57.0	236	11	Q9I237	Q9i237 mus musculu
36	45	57.0	441	10	Q38965	Q38965 arabidopsis
37	45	57.0	772	10	Q9LSE3	Q9lse3 arabidopsis
38	44	55.7	289	11	Q8R3Y8	Q8r3y8 mus musculu
39	44	55.7	361	4	Q9Y4P4	Q9y4p4 homo sapien
40	44	55.7	515	4	Q9BRZ9	Q9brz9 homo sapien
41	44	55.7	565	11	Q8BJC9	Q8bjc9 mus musculu
42	44	55.7	584	4	Q8IU81	Q8iui8 homo sapien
43	44	55.7	584	11	Q8CI76	Q8ci76 mus musculu
44	44	55.7	584	11	Q8COB1	Q8cob1 mus musculu
45	44	55.7	721	12	Q91LL5	Q91ll5 white spot

ALIGNMENTS

RESULT 1

Q9BPE9	PRELIMINARY;	PRT;	64 AA.
ID Q9BPE9			
AC Q9BPE9			
DT 01-JUN-2001 (TrEMBLrel. 17, Created)			
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE Conotoxin scaffold IX.			
OS Conus pennaceus (feathered cone).			
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;			
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;			
OC Neogastropoda; Conoidea; Conidae; Conus.			
OX NCBI_TaxID=37335;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21105969; PubMed=11158371;			
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,			
RA Fainzilber M.;			
RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";			
RL Mol. Biol. Evol. 18:120-131(2001).			
DR EMBL; AF214980; AAG60408.1; -			
DR GO; GO:0005576; C:extracellular; IEA.			
DR GO; GO:0015070; F:toxin activity; IEA.			
DR InterPro; IPR004214; Conotoxin.			
DR Pfam; PF02950; Conotoxin; 1.			
SQ SEQUENCE 64 AA; 6928 MW; 0AB87620FCCC1410 CRC64;			

Query Match 79.7%; Score 63; DB 5; Length 64;
Best Local Similarity 66.7%; Pred. No. 0.005;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVCCGYKLCFPC 12

Db 52 STCCGYRMCVPC 63

RESULT 2

Q9IBQ9

```
ID Q91B09 PRELIMINARY; PRT; 244 AA.
AC Q91B09;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF138 iso.
OS Spodoptera exigua nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10454;
RN [1]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=97437494; PubMed=9292027;
RA van Strien E.A., Faktor O., Hu Z.H., Zuidema D., Goldbach R.W.,
RA Vlask J.M.;
RT "Baculoviruses contain a gene for the large subunit of ribonucleotide
reductase.";
RL J. Gen. Virol. 78:2365-2377(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20036646; PubMed=10567663;
RA IJkel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,
RA Goldbach R.W., Vlask J.M.;
RT "Sequence and organization of the spodoptera exigua multicapsid
nucleopolyhedrovirus genome.";
RL J. Gen. Virol. 80:3289-3304(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX Zuidema D.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA IJkel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D.,
RA Goldbach R.W., Vlask J.M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169823; AAF33667.1; -.
DR InterPro; IPR007954; Baculo IE-1.
DR InterPro; IPR001841; Znf ring.
DR Pfam; PF05290; Baculo IE-1; 1.
DR SMART; SM00184; RING_1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 244 AA; 28719 MW; 1F7662E837A866DB CRC64;

Query Match 68.4%; Score 54; DB 12; Length 244;
Best Local Similarity 70.0%; Pred. No. 0.41;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGYKLCFFPC 12
Db 199 CCGYNLCYVC 208

RESULT 3
Q80LS1 PRELIMINARY; PRT; 243 AA.
AC Q80LS1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IB-0.
OS Adoxophyes honmai nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=224399;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ADN001;
RA Nakai M., Goto C., Kang W., Shikata M., Kunimi Y.;
RT "Sequence and genome organization of a nucleopolyhedrovirus isolated
from the smaller tea tortrix, Adoxophyes honmai.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006270; BAC67276.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
```

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DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR007954; Baculo IE-1.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001841; Znf ring.
DR Pfam; PF05290; Baculo IE-1; 1.
DR PROSITE; PS00190; CYTOCHROME C; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 243 AA; 28756 MW; 5D72075190E974A5 CRC64;

Query Match 67.1%; Score 53; DB 12; Length 243;
Best Local Similarity 60.0%; Pred. No. 0.6;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGYKLCFFPC 12
Db 209 CCGYSICYSC 218

RESULT 4
Q36453 PRELIMINARY; PRT; 258 AA.
AC Q36453; Q9YMW3;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Immediate early 0 protein (Immediate early transactivator 0).
GN IE-0.
OS Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97445059; PubMed=9300047;
RA Pearson M.N., Rohrmann G.F.;
RT "Splicing is required for transactivation by the immediate early gene
1 of the Lymantria dispar multinucleocapsid nuclear polyhedrosis
virus.";
RL Virology 235:153-165(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99124785; PubMed=9887315;
RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
RA Slavicek J.M., Rohrmann G.F.;
RT "Sequence and analysis of the genome of a baculovirus pathogenic for
Lymantria dispar.";
RL Virology 253:17-34(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
RA Slavicek J., Rohrmann G.F.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Kuzio J.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006656; AAC58234.1; -.
DR EMBL; AF081810; AAC70206.1; -.
DR PIR; T30368; T30368.
DR InterPro; IPR007954; Baculo IE-1.
DR InterPro; IPR001841; Znf ring.
DR Pfam; PF05290; Baculo IE-1; 1.
DR SMART; SM00184; RING_1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 258 AA; 29395 MW; AC564CDF92282BAD CRC64;

Query Match 67.1%; Score 53; DB 12; Length 258;
Best Local Similarity 58.3%; Pred. No. 0.63;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVCCGYKLCFFPC 12
Db 207 NVCCGYRVCNAC 218
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DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 151 AA; 17548 MW; 4986432F6DCD3169 CRC64;

Query Match 63.3%; Score 50; DB 12; Length 151;
Best Local Similarity 70.0%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGYKLCFFPC 12
DB 101 CCGYKICNLC 110

RESULT 7
Q8V5X4
ID Q8V5X4 PRELIMINARY; PRT; 285 AA.
AC Q8V5X4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF8.
OS Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10468;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F.,
RA Presnail J.K., Herrmann R., Dolan M., Tingey S., Hu Z.-H., Vlak J.M.;
RT "Genome sequence analysis of Helicoverpa zea single nucleocapsid
RT Nucleopolyhedrovirus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334030; AAL56153.1; -.
DR InterPro; IPR007954; Baculo IE-1.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF05290; Baculo IE-1; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 285 AA; 33189 MW; EF9E35A71B8E7F3D CRC64;

Query Match 63.3%; Score 50; DB 12; Length 285;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGYKLCFFPC 12
DB 235 CCGYKICNLC 244

RESULT 8
Q99H38
ID Q99H38 PRELIMINARY; PRT; 285 AA.
AC Q99H38;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE IE-0.
OS Helicoverpa armigera nucleopolyhedrovirus G4, and
OS Helicoverpa armigera nuclear polyhedrosis virus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=148363; 51313;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
RA Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;
RT "Sequence analysis of the gp37 gene of Heliothis armigera single-
RT nucleocapsid nucleopolyhedrovirus.";
RL Zhongguo Bingduxue 15:35-42(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
RA Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;
RT "Sequence analysis of the iap3 gene of Heliothis armigera single-
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RT nucleocapsid nucleopolyhedrovirus.";
RL Zhongguo Bingduxue 15:43-49(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
RX MEDLINE=21078302; PubMed=11210934;
RA Wang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.;
RT "Nucleotide sequence and transcriptional analysis of a putative basic
RT DNA-binding protein of Helicoverpa armigera polyhedrovirus.";
RL Virus Genes 22:113-120(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
RX MEDLINE=21064569; PubMed=1125177;
RA Chen X., IJkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
RA Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;
RT "The sequence of the Helicoverpa armigera single-nucleocapsid
RT nucleopolyhedrovirus genome.";
RL J. Gen. Virol. 82:241-257(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
RA Chen X., IJkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
RA Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=CI;
RX PubMed=12050807;
RA Zhang C.X., Wu J.C.;
RT "genome structure and the p10 gene of the Helicoverpa armigera
RT nucleopolyhedrovirus.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 33:179-184(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=CI;
RA Zhang C.X., Jin W.R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF271059; AAK53751.1; -.
DR EMBL; AF303045; AAK96301.1; -.
DR InterPro; IPR007954; Baculo_1E-1.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF05290; Baculo_1E-1; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
SQ SEQUENCE 285 AA; 33186 MW; C5FC3AB65BA27BDD CRC64;

Query Match 63.3%; Score 50; DB 12; Length 285;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGYKLCFCPC 12
Db 235 CCGYKICNLC 244

RESULT 9
Q9LD86 PRELIMINARY; PRT; 514 AA.
AC Q9LD86;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AT4G11390.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
SQ SEQUENCE OF 1-167 FROM N.A.
Bevan M., Robben J., Grymoprez B., Volckaert G, Bancroft I.,

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RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050399; CAB82144.1; -.
DR EMBL; AL161531; CAB81240.1; -.
DR PIR; T10559; T10559.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR004146; DC1_
DR InterPro; IPR000433; Znf_ZZ.
DR Pfam; PF03107; DC1; 2.
DR SMART; SM00109; CI; 3.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS01357; ZF_ZZ_1; 1.
KW Hypothetical protein_ZZ_1;
SQ SEQUENCE 514 AA; 59336 MW; B05CF4148B9D872F CRC64;

Query Match 63.3%; Score 50; DB 10; Length 514;
Best Local Similarity 70.0%; Pred. No. 3.3;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGYKLCFCPC 12
Db 295 CCGFVLCFC 304

RESULT 10
Q9M2P5 PRELIMINARY; PRT; 428 AA.
AC Q9M2P5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN T10K17.240.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Wurmbach E., Drzonek H., Ansorge W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AL132977; CAB67631.1; -.
DR PIR; T46025; T46025.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 428 AA; 47856 MW; D5F832A2E7BC16C8 CRC64;

Query Match 62.0%; Score 49; DB 10; Length 428;
Best Local Similarity 60.0%; Pred. No. 4.1;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGYKLCFCPC 12
Db 145 CCGHLYCWPC 154

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RESULT 11
ID Q8XFF2 PRELIMINARY; PRT; 436 AA.
AC Q8XFF2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (At3g58030).
GN AT3G58030.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
RA Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; A081289; AAL91178.1; -.
DR EMBL; BT006585; AAP31329.1; -.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 436 AA; 48703 MW; 5E72EC18C2EA4A2F CRC64;

Query Match 62.0%; Score 49; DB 10; Length 436;
Best Local Similarity 60.0%; Pred. No. 4.2;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCGYKLCFCPC 12
Db 153 CCGHLYCWPC 162

RESULT 12
ID Q7XIF9 PRELIMINARY; PRT; 2259 AA.
AC Q7XIF9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chromodomain helicase DNA binding protein-like protein.
GN P0005E02.107.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;

"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
clone: P0005E02.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004259; BAC79716.1; -.
SQ SEQUENCE 2259 AA; 251175 MW; 70D2167D74B55EAE CRC64;

Query Match 60.8%; Score 48; DB 10; Length 2259;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVCCGYKLCFCPC 12
Db 715 SLCCRYKINLPC 726

RESULT 13
ID Q9MIF9 PRELIMINARY; PRT; 373 AA.
AC Q9MIF9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN F9K21.60.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Jordan N., Bangert S., Wiedelmann R., Voss H., Unseid M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138657; CAB75477.1; -.
DR PIR; T47488; T47488.
DR InterPro; IPR002867; Znf_C6HC.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF01485; IIR; 2.
DR SMART; SM00647; IIR; 1.
DR SMART; SM00184; RING; 2.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00518; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 373 AA; 42686 MW; A4484B5BF00667BB CRC64;

Query Match 59.5%; Score 47; DB 10; Length 373;
Best Local Similarity 66.7%; Pred. No. 7.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCGYKLCFCPC 12
Db 329 CCGYKFCYAC 337

RESULT 14
ID Q9FWN3 PRELIMINARY; PRT; 470 AA.
AC Q9FWN3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T28K15.13 protein.
GN T28K15.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;

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Matches7;Conservative0;Mismatches2;Indels0;Gaps0;

QY4CGYKLCFPC12

DB433CGYVLCFDC441

Search completed: August 10, 2004, 16:04:23

Job time: 11.8649 secs

[1]SEQUENCE FROM N.A.

RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,

RA Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,

RA Buehler E., Chao C., Chin C., Chioi J., Choi E., Gonzalez A.,

RA Howg B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,

RA Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,

RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.,

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC022522; AAG12580.1; -

DR PIR; C86256; C86256.

DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

DR GO; GO:0004497; F:monooxygenase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000759; Adrndx_reductase.

DR InterPro; IPR001327; FAD pyr_redox.

DR InterPro; IPR000960; Flav cont_mnoxgn.

DR InterPro; IPR000205; NAD BS.

DR Pfam; PF00743; FMO-like; 1.

DR PRINTS; PR00419; ADXRDTASE.

DR PRINTS; PR00368; FADPNR.

DR PRINTS; PR00370; FMOXYGENASE.

SQ SEQUENCE 470 AA; 53837 MW; 6345C99AE5110919 CRC64;

Query Match 59.5%; Score 47; DB 10; Length 470;

Best Local Similarity 77.8%; Pred. No. 9.3;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY3CGYKLCFPC11

DB283CTGYKYCFPC291

RESULT 15

Q9LEB5PRELIMINARY;PRT;525 AA.

AC Q9LEB5; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN AT4G11540.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,

RA Mewes H.W., Lemcke K., Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL050399; CAB82159.1; -

DR EMBL; AL161532; CAB78197.1; -

DR PIR; T10574; T10574.

DR GO; GO:0005489; F:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

DR InterPro; IPR000345; CytC_heme_BS.

DR InterPro; IPR002219; DAG_PE-bind.

DR InterPro; IPR004146; DC1.

DR Pfam; PF03107; DC1; 3.

DR SMART; SM00109; C1; 4.

DR PROSITE; PS00190; CYTOCHROME_C; 2.

KW Hypothetical protein.

SQ SEQUENCE 525 AA; 60740 MW; 069557044AB56D4A CRC64;

Query Match 59.5%; Score 47; DB 10; Length 525;

Best Local Similarity 77.8%; Pred. No. 10;